GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

June 9, 1999, 10:26:01; Search time 23.43 Seconds Run on:

(without alignments) 178.687 Million cell updates/sec

US-08-486-814-17

Perfect score: Title:

1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Sequence:

BLOSUM62 Scoring table: 162890 segs, 20225328 residues Searched:

A_Geneseq_34:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	A transact	d-type E.coli	i-chimeric	i-chimeric t	rote	ence of the	transacti	nsactiv	TIASMIN PASK OPE	rin hom	tTA transactivator	k er	d Tet	Tet	Tet	ī.	Tet	ed Tet	Tet repre	Mutated Tet repres	Tet repre	Total	Tn-1	Tn-10	reve	Tet	Tet	Tet	enco	enco.	Tet		Tet I	Tet r	ed Tet r	ted Tet r	ted Tet r	ted Tet repr	ted Tet repr	Mutated Tet repres
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ď	Query Match	90	000	80	8	00	•	•	•	•	•	•		-		- 3											-	~	~	~	~	•	~	~	~	~	^	7	\sim	_	_
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WO9601313-A1. 18-JAN-1996. 29-JUN-1995; U08179. 01-JUL-1994; US-270637.

Transposon In-10.

transcription

Seg. Tbs (7*19 08/241347 のとってら

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Mutated Tet repres
Mutated Tet repres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulatory systems using tetracycline-controllable transactivator (tTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal bisclosure; page 46-48; 103pp; Bnglish coding for the C-terminal 130 amino acids of VP16 of HSV was blunted and inserted in pUHD14-1. The resulting plasmid, pUHD15-1, encoded a tetR-VP16 fushon protein, or tetracycline-controllable transactivator (tTA), whose sequence is Sequence 335 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-1996 (first entry)
Wild type Tn-10 derived Tet repressor.
Tet repressor; Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
                                                                                                                                                                                     tTA; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR; transgenic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1080; DB 1;
100.0%; Pred. No. 1.2e-112;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             rd H, Gossen M, Salfeld JG, Voss JW;
95-036472/05.
                                                            ALIGNMENTS
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W08309
W08311
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                                                                                                                                     R64808 standard; Protein; 335 AA.
                                                                                                                                                                                                                                                       Herpes simplex virus K12, KOS WO9429442-A
                                                                                                                                                                   17-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 207; Conservative
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14-JUN-1994; U06734.
14-JUN-1993; US-076327.
(BADI ) BASF AG.
   207
                                                                                                                                                                                   tTA transactivator.
   97.6
97.6
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N-PSDB; Q76264.
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R89763
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inhibit transcription

'G claim 38: Page 78: 112pp; English.

Fusion proteins comprising a first polypeptide which binds to a tet

C rusion proteins comprising a first polypeptide which binds to a tet

C rusion proteins comprising a first polypeptide which binds to a tet

C coperator sequence in the presence of tetracycline or a tetracycline

C analogue, operatively linked to a second polypeptide which either

C analogue, operatively linked to a second polypeptide which either

C cotivates or inhibits transcription in eukaryotic cells may be used

C octivate or inhibit transcription. Such proteins may be used

C octivate or inhibit transcription of gene products in transgenic

C gene therapy and for expression of gene products in transgenic

C reganisms. Induction of gene expression is rapid, efficient and

Strong, typically 1000-2000 fold. The inducing agent does not cause

C pleitropic effects or cytotoxicity in eukaryotic cells. This

Sequence is the wild type Tn-10 tet repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 97-052305/05.

Nucleic acid encoding tetracycline-inducible transcription regulatory fusion protein - comprising modified tetracycline regulatory fusion protein - comprising modified tetracycline repressor able to bind mutant tet operator, fused to transcription regulator, useful for modulating eukaryotic gene expression Example 4, Page 84.85; IJ7pp; English.

W08236 represents wild-type Tet repressor (TetR) protein, derived from transposon 10 (Tn10) of E. coli. The wild-type sequence is used for the production of a mutated TetR (e.g. so as to bind its target in the presence rather than the absence of tetracycline). Mutant TetR proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1997 (first entry)
Wild-type E.coli In10-derived Tet repressor.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1080; DB 1; Length 207; 100.0%; Pred. No. 5.9e-113; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 207; Conservative
15-JUL-1994; US-275876.
03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
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07-JUN-1995; US-485971.
(BADI ) BASF AG.
                                                                                                        Bujard H, Gossen M;
WPI; 96-087666/09.
N-PSDB; T11351.
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Best Local Similarity
                                                              (BUJA/) BUJARD H.
(GOSS/) GOSSEN M.
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WO9640892-A1.
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can be fused to a transcriptional activator e.g. VP16 (herpes simplex virus virion protein 16), to form a TC-controlled transcriptional activator (trah). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator sequences tetO-4C and tetO-6C (see T45711 and T48478). Modified TetR proteins can be fused to any transcription regulatory polypeptide and used to control transcription of a tetO-4C or tetO-6C linked gene. Nucleic acid encoding such a fusion protein may be introduced into a cell and transcription of the protein can be controlled by altering the control of the protein can be controlled by altering the control of the protein can be controlled by altering the control of the protein can analogue) in the cell, as appropriate. This ability to modulate gene expression in a predictable way is very useful in gene therapy and for recombinant protein prodn. in cultured calls or transgenic animals. The Tc-inducible system is also useful for the prodn. of transgenic animal models for the study of gene function e.g. during differentiation. The Tc-inducible system allows rapid activation of gene transcription cannon controllar by the control of the required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New packaging cell lines for pseudotyped retroviral vectors comprises sequences encoding retroviral Gag and Pol polypeptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig. 4A-C; 84pp; English.
This fusion protein comprises a multi-chimeric transactivator,
designated rTAER, that is composed of (from the N-terminus to the
C-terminus) the Escherichia coli teta polypeptide, the
transcriptional activation domain of herpes simplex virus VP16, an
the ligand binding domain of the oestrogen receptor. An inducible
expression system of the invention is composed of tTAER and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 1080; DB 1; Length 207; Local Similarity 100.0%; Pred. No. 5.9e-113; nes 207; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multi-chimeric transactivating factor rTAER fusion protein.
Multi-chimeric transactivating factor; rTAER; tetR;
tetracycline repressor; HSV; oestrogen receptor; promoter;
packaging cell line; retrovirus; retroviral particle; vector;
gene delivery; gene therapy.
Chimeric - Bscherichia coli.
Chimeric - Herpes simplex virus.
Chimeric - Mammalla.
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06-AUG-1997; U13846.
06-AUG-1996.
CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
Chen S, Friedmann T, Miyanohara A, Prussak CE, Yee J;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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transcriptional activation. Sequence 651 AA;

Sequence

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New inducible expression systems - comprising multi-chimeric

New inducible expression systems - comprising multi-chimeric

Transactivator, induces transcription from promoter in the absence
of first ligand and presence of second ligand

Frample 1; Fig 4; 72pp: English.

Example 1; Fig 4; 72pp: English.

This is a fusion protein comprising, from N-terminus to C-terminus,
the E.coli tetR polypeptide, the transcription activational domain

the E.coli tetR polypeptide, the transcription activational domain

from pHE14 (Kumar et al. 1986). DNA encoding it can be used as part of
an inducible expression system which induces transcription from the
conductr in the absence of the first ligand and presence of the
second. The products can be used for the inducible expression in cells
of polypeptides such as cytotoxic products or therapeutic products.

The activation of the inducible expression system requires 2
independent signals, which reduces the incidence of undesired
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
minimal promoter (see V17755) derived from the immediate early gene of cytomegalovirus linked to 7 tandem copies of the tet operator (teto) that is the binding site for tetk, which in turn can be linked to a nucleotide sequence of interest. The invention relates to perferably (f27h cells and recombinant retroviral particles. Crowleded by them, particularly pseudotyped retroviral particles. Perroviral particles are produced by inducibly expressing an envelope protein-encoding nucleotide sequence to the inducible expression in cells of polypeptides, can be cytotoxic products or therapeutic agents. The activation of the inducible expression in cells of polypeptides, e.g. cytotoxic products or therapeutic agents. The activation of the inducible expression in cells of polypeptides, e.g. cytotoxic products or therapeutic agents. The activation of the inducible expression requires 2 independent signals, thus reducing the incidence of undesired transcriptional activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inducible expression system; modulation; cytotoxin; therapeutic; transR; multi-chimeric; transactivator; tetR; Vp16;
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1080; DB 1; Length 651; 100.0%; Pred. No. 2.9e-112; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multi-chimeric transactivator tTAER sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              207; Conservative
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07-AUG-1996; US-693940.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligand-binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    651 AA;
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claim 4: Columns 77-80; 63pp; English.

Claim 4: Columns 77-80; 63pp; English.

The present sequence is encoded by wild type Th10-derived tet repressor.

The present sequence of the invention. The specification describes a

It is used in the course of the invention. The specification describes a

claim in a cell of a subject. The method comprises introducing into the

cell a nucleic acid encoding a fusion protein which inhibits

transcription in eukaryotic cells, the fusion protein comprising a

polypeptide which binds to a Tet operator sequence, operatively linked

to heterologous second polypeptide which inhibits transcription in

eukaryotic cells and modulating the concentration of a tetracycline

(analogue) in the subject. The method is used for the regulation of

gene expression system, using tetracycline (analogues). The system

canables a gene coupled to the system to be induced in the presence of

Tet and then stopped when Tet is removed.
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                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                     Gaps
                                                             1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Length 651;
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protein encoded by wild type Tnl0-derived tet repressor.
Tet repressor; tetracycline; regulation; expression;
Tet operator-linked gene; tet operator.
                                Indels
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100.0%; Pred. No. 5.9e-113;
tive 0; Mismatches 0;
100.0%; Score 1080; DB 1; 100.0%; Pred. No. 2.9e-112;
                                ;
          100.0%; Pred. ...
                                                                                                                                                                                                                                                                             181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                               W71326 standard; Protein; 207 AA.
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Best Local Similarity 100.0
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995; US-485978.
14-JUN-1993; US-076327.
14-JUN-1993; US-076327.
14-JUN-1994; US-270657.
01-JUL-1994; US-270637.
15-JUL-1994; US-270637.
06-FEB-1995; US-383754.
(RNOL.) KNOLL AG.
                                  Matches 207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bujard H, Gossen M;
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                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V60088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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   Query Match
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17-JUL-1995

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                                                                            61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                     121 CQOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetracycline repressor-mediated regulation system - useful for controlling gene expression in transpenic animals
Disclosure; page 41-42; 76pp; English.
The inventors claim a construct which comprises an animal promoter element having a tetracycline repressor (tetR) operator. The promoter element having a tetracycline repressor (tetR) operator. The being the promoter promoter element may be the PEPCK promoter which is tissue specific shortly prior to birth. The tetR sequence in the construct is 3' to a TATA-box sequence and is inserted into the Nher site of the PEPCK promoter element. The entire sequence of the tetR Sequence 207 AA;
1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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Pred. No. 2.1e-112;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                               19-A0G-1994 (first entry)
Sequence of the tetracycline repressor tetR.
Tetracycline repressor: TetR: Tn10; transposon 10.
                                                                                                                                                                                181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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99.5%;
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26-AUG-1992; US-935763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94-083191/10.
                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                             WO9404672-A.
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WPI; 94-0
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tTA; tTAS; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR; transgentc animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulatory systems using tetracycline-controllable transactivator (TTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal bisclosure; Page 50-51; 103pp; English.
A DNA fragment of pwsypl6 coding for the C-terminal 97 amino acids of VP16 of HSV was blunted and inserted in pwlD14-1. The resulting plasmid, pUHD151-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (smaller version, tTAs), sequence 197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding trans:activator fusion protein contg. tet repressor - used to control expression of gene regulated by minimal promoter linked to tet operon, and vectors and cells where gene expression is regulated by tetracycline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tTAS transactivator.
Transactivator; tTAS; tet repressor; tetR; virion protein 16; VP16;
gene expression; tetracycline-responsive promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%; Score 1075; DB 1; Length 297; 99.5%; Pred. No. 3.5e-112; tive 0; Mismatches 1; Indels
                                                                                                                                                                         (BADI ) BASF AG.
Waljard H. Gossen M, Salfeld JG, Voss JW;
WPI; 95-036472/05.
N-PSDB; Q76265.
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                                                                                               Herpes simplex virus K12, KOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic animal.
Chimeric Escherichia coli;
Chimeric Herpes simplex virus.
USS464758-A.
   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206; Conservative
                                                                                                                                           14-JUN-1994; U06734.
14-JUN-1993; US-076327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-1995.
14-JUN-1993; 076726.
14-JUN-1993; US-076726.
                  tTAs transactivator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T06868.
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A fusion protein (R85324) composed of the Escherichia coli Tn10 tet repressor (tetR) and a 127-amino acid C-terminal portion of the transcription activating domain of herpes simplex virus virion protein 16 (VP16) is the product of novel tetracycline-controlled transactivator tTA (T06868). The transactivator is used to regulate expression of a heterologous gene operably linked to a minimal promoter derived from human cytomegalovirus promoter IE (see T06869-70) and at least 1 tet operator (tetO) sequence. On/Off regulation of expression of the heterologous protein by host eukaryotic cells is provided by varying the medium tetracycline conc. Transgenic animals producing a desired protein in their milk can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prokaryour vector for regulated prodn. of heterologous protein gene controlled by promoter repressed by tetracycline repressor protein, prodn. of which is controlled by independent promoter not regulated by this repressor Disclosure: Fig la; 50pp; German. Plasmid paksn5 is a specifically claimed example of a prokaryotic expression vector comprising the tetracycline promoter/operator (P/O) region and the tetracycline repressor (tetR) gene. The tetR gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                               0; Gaps
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27-JUN-1996 (first entry)
Plasmid pASK75 open reading frame (c) translation.
Tetracycline; resistance; TetR gene; repressor protein; TetA gene;
prokaryotic expression vector; beta-lactamase promoter; bla gene;
circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "each X corresponds to a termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="C-terminal end of beta-lactamase, the exact position of the N-terminus is not given in the specification"
                                                                                                                                                                                                                                                                                   99.5%; Score 1075; DB 1; Length 297; 99.5%; Pred. No. 3.5e-112; tive 0; Mismatches 1; Indels (
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
Skerra A, Wardenberg C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         614. .820 -
/label- TetR
/note= "tetracycline repressor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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/note= "e
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                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                       Query Match
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Controlling expression of insecticidal proteins - using recombinant baculovirus containing tetracycline trans:activator protein Example 2; Fig 8; 65pp; English.

This transactivator protein is encoded by a hybrid gene consisting of the tetracycline repressor gene (tetR) of E. coli (174611) fused in frame with the immediate early promoter (FERA) of Baculovirus (T74614). The protein is used to demonstrate a novel method of gene expression regulation of recombinant baculoviruses in an insect cell/host. An insect cell is constructed having a chimeric gene, which consists of a promoter (e.g. T74614) operably linked to DNA encoding a regulatory protein capable of affecting gene expression. The regulatory protein capable of affecting gene expression. The regulatory protein baculovirus expression vector is then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                             61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   under the control of the heta-lactamase (bla) promoter. Expression of heterologous genes inserted downstream of the tet P/O is controlled by the activity of the Tet repressor. Plasmid pASK75 was derived from pASK60-Strep (Schmidt and Skerra, Frotein. Eng. 6 (1993), 109-122) and further contains the OmpA leader peptide coding sequence, a polylinker and a strepthfidin binding peptide strep-tag coding region from the parent plasmid. In addition, pASK75 contains the ColEl origin of replication, the bla geit, intergene regions of filamentous phage fl and a lipoprotein terminator. The specification includes the translated sequences from all three regions are all in reading frame (c).
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                        Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetracycline transactivator fusion protein tetrIEIA.
Baculovirus; recombinant protein; neurotoxin; parasite;
biological control; insecticide; insecticidal protein;
nuclear polyhedrosis virus; early promoter; tetracycline.
                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                        99.5%; Score 1075; DB 1; 99.5%; Pred. No. 2.2e-111;
                                                                                                                                                                                                                                                                                                                               0; Mismatches
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/label= "IE1A peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1995; US-009120.
(DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W21994 standard; Protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W21994;
26-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                     Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Baculovirus.
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-1997.
16-DEC-1996; U20512.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCutchen BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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constructed. This has a second chimeric gene, which consists of a promoter (one or more tetracycline operator sites operably linked to a minimal promoter region, see T14615-16) that is affected by the above regulatory protein. This promoter is operably linked to DNA encoding an insecticidal protein, (W21993). The recombinant baculovirus expression fusector is introduced into the recombinant insect cell. Expression of the recombinant insect cells and the recombinant baculoviruses may be used in the production of insecticidal recombinant baculoviruses may be used in the production of insecticidal recombinant baculoviruses. Insect cells treated with recombinant viruses, as described, show an increase in the Sequence 354 AA;
         88388888888888
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                                                                                                                      61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                        121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                      0; Gaps
                                                          1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                            99.5%; Score 1075; DB 1; Length 354; 99.5%; Pred. No. 4.5e-112; 1ve 0; Mismatches 1; Indels (
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                Best Local Similarity 99.5
Matches 206; Conservative
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Example 4; Page 79-81; 137pp; English.

This polypeptide comprises a fusion between a synthetic Pleckstrin homology (PH) domain (see W54285) of human cythohesin 1 and a tet repressor. It is encoded by plasmid pTLP2 (see V26524). The fusion protein is expressed from a polycistronic message, constitutively transcribed from the beta-lactamase promoter. The plasmid was used to transform Escherichia coli JM109 cells. The construct was used to demonstrate the folding, stability, functionality and ease of handling of a fusion protein comprising a synthetic PH domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V26524.
Vectors used to produce PH domain-like peptide libraries - which are
screened for therapeutically useful peptide(s), e.g. to produce
                                                            28-AUG-1998 (first entry)
Pleckstrin homology domain-tet repressor fusion.
Pleckstrin homology domain; PH domain; peptide library;
functional molecular surface; protein structural template;
vaccine; gene therapy; cytohesin 1; human; plasmid pTLP2;
                                                                                                                                                                                                                                                1. .221
/label= Tet_repressor
                                                                                                                                                                                                                                                                                                                                               30-MAY-1997; E02840.
31-MAY-1965; EP-108776.
(MEDI-) MEDIGENE AG.
Bruhn H, Funk M, Henkel T, Steipe B;
WPI: 98-230215/20.
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                /label= PH_domain
                                W54311 standard; Protein; 349 AA.
                                                                                                                                                                         Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                WO9745538-A1.
                                                                                                                                                                                                                                                                                                                                    04-DEC-1997
                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccines
                                                                                                                                                                                                                                              Protein
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RESULT 12
W54311
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Gaps

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99.4%; Score 1073; DB 1; Length 335; 99.5%; Pred. No. 7e-112; tive 0; Mismatches 1; Indels (

Matches 206; Conservative

Query Match Best Local Similarity

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Polynucleotide encoding trans:activator fusion protein contg. tet
Polynucleotide encoding trans:activator fusion protein contg. tet
Polynucleotide encoding trans:activator of gene regulated by minimal
Promoter linked to control expression of gene regulated by minimal
Promoter linked to tet operon, and vectors and cells where gene
Promoter linked to tet operon, and vectors and cells where gene
Promoter linked to tet operon, and vectors and cells where gene
Promoter linked to tet operon and vectors and cells in the
Polynucle of the Escherichia coli Th10
Let repressor (tetR) and a 127-amino acid C-terminal portion of the
Protein 16 (VP16) is the product of novel tetracycline-controlled
Protein 16 (VP16) is the product of novel tetracycline-controlled
Protein 16 (VP16) is the product of novel tetracycline-controlled
Protein 16 (VP16) is the product of novel tetracycline-controlled
Protein 16 (VP16) is the product of novel tetracycline controlled
Protein 16 (VP16) is the product of novel tetracycline conc. Transgenic animals producing
Protein 16 (VP16) is the firmilk can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTERQYETLENQLAFL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                    .61
a DNA binding domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, especially novel binding or catalytic properties, and which may be of use in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and sevolution of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                           2 MSKLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transactivator; tTA; tet repressor; tetR; virion protein 16; VP16;
                                                                                                                                                                                                                                                                                                                     1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
                                                                                                                                                                                                                                     Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression; tetracycline-responsive promoter;
                                                                                                                                                                                                                                   99.5%; Score 1075; DB 1;
99.5%; Pred. No. 4.4e-112;
iive 0; Mismatches 1;
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Chimeric Herpes simplex virus.
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tTA transactivator.
                                                                                                                                                                                                                                                                           Matches 206; Conservative
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07-NOV-1995.
14-JUN-1993; 076726.
14-JUN-1993; US-076726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bujard H, Gossen M;
WPI; 95-392612/50.
                                                                                                                                                                                                                                                         Similarity
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(GOSS/) GOSSEN M.
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                                                                  Gaps
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1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; 749877.

N-PSDB; 749877.

N-PSDB; 749877.

N-Notlaic acid encoding tetracycline transactivator fusion protein provides rapid and reversible control of gene expression, e.g. for creating animal models for drug screening

Example 1; Fig 10b-g; 82pp: English.

Autoregulatory plasmid pret-trak (749877) contains a modified tetracycline transactivator gene, t7Ak, under control of a minimal promoter. It encodes a 365-mino acid protein (W08474). An autoregulatory tetracycline-regulated system for inducible gene expression in eukaryotes has been developed that allows the rapid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reversible control of gene expression in eukaryotic cells, and creation of transgenic animals in which expression of a luciferase reporter gene is controlled by altering the concentration of tetracycline in the drinking water of the animals.
               121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ
                                                                                                                                                                                                                                                                                 28-MAR-1997 (first entry)
pret-trak enceded protein:
pret-trak; pret-Splice; tetracycline transactivator; promoter;
pret-trak; pret-Splice; tetracycline transactivator; promoter;
gene expression; transgenic animal; animal model; drug screening.
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                                                                                                                                                              181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                         W08474 standard; Protein; 336 AA
                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996; U10109.
07-JUN-1995; US-474169.
(UXYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 97-077273/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Schatz DG;
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W08474
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Nucleic acid encounts terracycline-inducible refusivitybelong propertion acid encounts the comprising modified tetracycline regulatory fusion protein - comprising modified tetracycline regulator, useful for modulating eukaryotic gene expression claim 5: Page -: illpp: English.

Equilator, useful for modulating eukaryotic gene expression claim 5: Page -: illpp: English.

Common the comprision of the year of the comprision a mutated Tetk fused to a transcriptional control sequence (e.g. verbA silencer domain), to produce tetracycline (TO)-controlled transcriptional activators (TTA).

Common invention of the specification concerns modified Tetk proteins that bind to modified class B tet operator sequences teto-4C and teto-6C (see T45711 and T48478). Modified Tetk proteins can be fused to any transcription of a teto-4C or teto-6C linked gene. Nucleic acid concoling such a teto-4C or teto-6C linked gene. Nucleic acid concoling such a teto-4C or teto-6C linked gene. Nucleic acid concoling such a teto-4C or teto-6C linked gene. Nucleic acid concoling such a teto-4C or teto-6C linked gene. Nucleic acid concoling such a teto-4C or teto-6C linked gene.

Common for an analogue) in the cell, as appropriate. The ability to modulate gene expression in a predictable way is very useful an gene therapy and for recombinant protein prode in collured cells or transgenic animals. The Tc-inducible system allows rapid activation of gene transcription. The for the study of gene function e.g. during differentiation. The connect control of the control of inducer are not required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
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Mutated Tet repressor for Tet-inducible transcriptional regulator.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding tetracycline-inducible transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rd H, Gossen M, Helbl V, Hillen W, Schnappinger D;
97-052305/05.
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                                                                                                                                                                                                                                                                                 /note= "Lys replaces wild-type Glu" misc_difference 39
                                                                                                                                                                                                                                                                                                                                                                                                              "Gln replaces wild-type Pro"
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                                                                                                                                                                                                                                                                                                                                                                            /label= substitution
                                                                                                                                                                                                                           Location/Qualifiers
W08323 standard; Protein; 207 AA.
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Best Local Similarity 99.03
Matches 205; Conservative
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06-JUN-1996; U09049.
                                                                                                                                                                                                                                                         misc_difference 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9640892-A1.
                                        W08323;
21-MAR-1997
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                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bujard H,
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RESULT

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 9, 1999, 10:27:01; Search time 19.42 Seconds (without alignments) 399.294 Million cell updates/sec

US-08-486-814-17 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207

Title: Perfect score: Sequence:

116738 seqs, 37460341 residues

BLOSUM62

Scoring table:

PIR_58:* Database : Searched:

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	epressor t	protei	protei	e resi		atory prot			tet repressor prot	hetical p	esso	hypothetical prote				transcription regu	а.			transcription regu	ca.	probable regulato	transcription regu	conserved hypothet	iron-dependent rep		hypothetical prote		⊑		cal	O.	nitrogen fixation	ď	u	ξ,		5	transcription regu
SUMMERCES	DI	RPECTN	807359	S30287	A26948	RPECYS	JQ1478	S38655	177569	RPECR1	H70740	A40046	A69900	S42417	S42419	H70042	C70487	B70827	D64918	875298	B70391	E70861	F70946	C70035	A64695	E69280	S29308	D64855	I49045	E69779	S12393	H70001	C70649	S31136	S10899	S17885	F70487	F64995	A71023	S39744
	80																																							
	Length	207	218	218	126	219	216	216	211	216	261	259	191	210	210	189	192	196	196	236	179	246	213	194	235	192	205	236	677	198	188	207	216	519	195	365	192	260	629	299
dю	Query	99.	63.2	63.2	57.3	48.6	47.7	47.7	47.2	46.8	16.3	13.8	11.0	10.2	10.2	10.0	9.4	9.1	8.8	8.8	8.7	8.7	8.5	8.2	8.1	8.0	8.0	7.9	7.9	7.9	7.8	7.8	7.7	7.7	7.7	7.7	7.7	7.6	7.6	
	Score	1075												110.5					'n		94	93.5	٠,	88	87.5	9	98	85.5	S	85	84	84	83.5	83	83	83	83	82	82	81.5
	Result No.	;	7	m	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	. 37	38	39

nitrogen fixation hypothetical prote ttk protein - Esch hypothetical prote	repressor for cyto
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517 543 212 190	192
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hypothetical prote ttk protein - Esch hypothetical prote probable transcrip repressor for cyto	RESULT 1 RPECTN TEACRASOR TELE - Escherichia coli transposon Tn10 C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 12-Jun-1998 C;Accession: A03576; 802667 R;Postle, K.; Nguyen, T.T.; Bertrand, K.P. Nucleic Acids Res. 12, 4849-4863, 1984 A;Title: Nucleotide sequence of the repressor gene of the TN10 tetracycline resistanc A;Recession: A03576; MUID:84247342 A;Molecule type: DNA	A; Residues: 1-207 <ross \$02667="" \$02667;="" 1-100="" 1-207="" 1988="" 40="" 4011-4017,="" 7,="" <alt="" <ross="" a="" a;="" accession:="" alamine="" alters="" at="" atlaschmied,="" baumeister,="" dna="" embo="" exchange="" hillen,="" j.="" k.;="" l.;="" molecule="" muid:89091153="" number:="" of="" pfleiderer,="" position="" r="" r.;="" reference="" repressor="" residues:="" tet="" the="" threonine="" title:="" to="" type:="" w.=""> A; Residues: 1-100 <alt> A; Cross-references: \$(B:J01830; NID:9154845) C; Comment: This protein contains sequences similar to the DNA recognition regions of C; Generics:</alt></ross>	regulatio 207;	MSRLDKSKVINSALELLNEYGIEGITTRKLAQKLGVEQPTLYWHYKNRRALLDALAIEML 60	Oy 181 GAEPAFLFGLELIICGLEKQLKCESGS 207
S19005 S58095 C65165 S38906 E70873 A42116	ALIG transp transp rision 1 rand, K. 1984 the repr :8424734	in:94305; Pfleic exchange:8909116 eptual t	essor e; DNA] #status Score Pred. 0; Mil	EGLITER 	CESGS 2 CESGS 2 CESGS 2 CESGS 2 CESGS 2
00000	col: Lrev Sert: 1863	I; N. R. Ine MUID Conc	repr tanc elix elix .5%;	EVGI 	KOLK
217 212 190 187 192	richia coli colose colose rii.; E 4849-4 quence	%:X00694 neister, neister, co alan; 02667; h l with c	etracycline reprebiotic resistance helix-turn-helix 99.5%; ilarity 99.5%;	SALELLN SALELLN GESWQDF GESWQDF YALSAVG	GAEPAFLFGLELIICGLEKQLKCESGS
	- Esche erichia 1987 #s 1987 #s 3576; s 9uyen, es: 12, es: 12, tide se ber: AC	cos: GE 1.; Baun 1.; Baun 1.; Baun 1.; Baun 1.; Baun 1.; Baun 1.067 1.00 ALI 1.00 ALI 1.00 ALI	tetrac; iblotic; helix imilari; Cons;	OKSKVIN. DKSKVIN THFCPLE THFCPLE	AFLFGLE AFLFGLE tein te mes: te herichi herichi 07359 lock, G
80 80 80 80 80 80	or tetR ss: Esch sion: A0 sion: A0 si, K.; N Acids R nuclec ence num	les: 1-2 referen mmied, 1 7, 4011 : A thre ence num sion: SC s: not c ule type ules: 1-1 referer rt: This	Gene: tetR Superfamily: tetracyc Keywords: antibiotic 25-46/Region: helix-tr Ouery Match Best Local Similarity Matches 206; Conser	1 MSRLI 1 MSRLI 61 DRHH' 61 DRHH' 121 CQQG	181 GAEP 191 GAEP 2 2 101 GAEP 102 Pro 103 February pro 103 February pro 103 February pro 103 February pro 103 February pro 104 February pro 105 February pro 1
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT RPECTN C. Date: C. Date: C. Date: C. A. Title: A. Title: A. Macerre	A, Residu A, Cross R, Altscl EMBO J. A, Title A, Referc A, Acces; A, Statu A, Statu A, Cross A, Cross A, Cross C, Gomme	A, Gene: C, Super C, Keywo F, 25-46 Query Best Match	0.y 0.y 0.y 0.y 1 0.p	Oy 1 Db 1 RESULT SOTIAL SOTIAL N'Alter C'SPECI C'SPECI C'ACCES R'UNGER

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181 DGEQAFLHGLESLIRGFEVQL 201
                181 GAEPAFLFGLELIICGLEKQL 201
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A; Residues: 1-219 <BRO>
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Matches 119;
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F. Accession: 300207

F. Allard, J.D.; Gibson, M.L.; Vu, L.H.; Nguyen, T.T.; Bertrand, K.P.

Mol. Gen. Gibson, M.L.; Vu, L.H.; Nguyen, T.T.; Bertrand, K.P.

A. Title: Nucleotide sequence of class D tetracycline resistance genes from Salmonella or A. Reference number: 530286

A. M. Reference number: 530286

A. M. Molecule type: DNA

A. M. Residues: 1-218 < ALL.>

A. M. Residues: 1-218 < ALL.>

A. Cross-references: EMBL: X65876; NID:949073; PID:949075
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N.Alternate names: tetracycline repressor
C;Species: Salmonella ordonez
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                          61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
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                                                                                                                                  A Genome: plasmid
C:Superfamily: tetracycline repressor
C:Keywords: antibiotic resistance; DNA binding; transcription regulation
F:25-46/Region: helix-turn-helix *status predicted
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                                                                         A)Cross-references: EMBL:X01083; NID:g43053; PID:g43054
C;Genetics:
A;Gene: tetR
                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                     Query Match
63.2%; Score 683; DB 2;
Best Local Similarity 65.2%; Pred. No. 4.1e-56;
Matches 131; Conservative 26; Mismatches 44;
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65.2%; Pred. No. 4.1e-56;
tive 26; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Gene: tetR
A.Genome: plasmid
G.Superfamily: tetracycline repressor
C.Superfamily: tetracycline resistance; DNA binding; tre
C.Keywords: antibiotic resistance; DNA binding; tre
F;25-46/Region: helix-turn-helix #status predicted
Reference number: S07359; MUID:85037938
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Matches 131; Conservative
                                                       A; Residues: 1-218 <UNG>
                                          A; Molecule type: DNA
                      S07359
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tetracycline resistance protein - Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Dacte: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 12-Jun-1998
C;Accession: A26948
R;Heuer, C.; Hickman, R.K.; Curiale, M.S.; Hillen, W.; Levy, S.B.
A;Fitle: Constitutive expression of tetracycline resistance mediated by a Tn10-like A;Reference number: A26948; MUID:87137315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M36272; NID:g150945; PID:g150946
C;Comment: This protein is the repressor of the tetracycline resistance element; its
C;Genetics:
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C; Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residudes: 1-126 <HEU>
C;Genetics: GB:M15539; NID:g148988; PID:g148989
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C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
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C:Superfamily: tetracycline repressor
C:Reywords: antibiotic resistance; DNA binding; tran
F:24-46/Domain: DNA binding #status predicted C:25-46/Region: helix-turn-helix #status predicted
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Mol. Biol. Evol. 2, 1-12, 1985
A;Title: The tetracycline repressor of pSC101.
A;Reference number: A03575; MUID:88216101.
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179 HQGAEPAFLFGLELIICGLEKQ 200
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A; Reference number: S38655
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Best Local Similarity
                                                                     A; Molecule type: DNA
A; Residues: 1-216 <TRU>
                                              A; Status: preliminary
                         A; Accession: S38655
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A; Residues: 1-216 <aLL>
A; Residues: 1-216 <aLL>
A; Residues: 1-216 <aLL>
A; Residues: 1-216 <aLL>
A; Cross-references: EMBL:X61367; NID:g48194; PID:g48198
A; Note: the authors translated the codon GAG for residue 19 as Asp and CAG for residue 8
A; Note: the authors translated the codon GAG for residue 19 as Asp and CAG for residue 8
A; Altechmied, L.; Baumeister, R.; Pfleiderer, R.; Hillen, W.
EMBO J. 7, 4011-4017, 1988
A; Title: A threonine to alanine exchange at position 40 of tet repressor alters the recc
A; Reference number: S02667; MUID:89091153
A; Accession: S02668
                                                                                                                                                                                                                                                                                                                                                                                requiatory protein tetR - Escherichia coli transposon Tn1721
N.Alternate names: tetracycline resistance repressor
C.Species: Escherichia coli
C.Species: Bscherichia coli
C.Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 12-Jun-1998
C.Accession: J01478, S02668; S24113
R.Allmeier, H.; Cresnar, B.; Greck, M.; Schmitt, R.
Gene 111, 11-20, 1992
A.Title: Complete nucleotide sequence of Tn1721: gene organization and a novel gene prod
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Jun-1998
C;Accession: 53865;
R;Trueman, P.; Sharpe, G.S.; Barth, P.T.
submitted to the EMBL Data Library, November 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
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                                                                                                                                                        1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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                                                        121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
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                                                                                                                                                                                                                             177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                            181 VYEGGPDAAFERGLALIIGGLEK 203
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180 EAGPDAAFEQGLAVIVDGLAKR 201
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A;Residues: 1-100 <ALT>
C;Genetice:
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-0un-1996 #sequence_revision 07-Jun-1996 #text_change 12-Jun-1998
C;Accession: 177569
R;Tovar, K.; Ernst, A.; Hillen, W.
Mol. Gen. Genet. 215, 76-80, 1988
A;Title: Identification and nucleotide sequence of the class E tet regulatory element
A;Reference number: 157766; MuDi:89201249
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                                                                                                                                                                                                                             1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                           1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
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51.2%; Pred. No. 4.4e-40;
tive 29; Mismatches 66; Indels 3;
                                                                                                                                 Length 216;
A;Cross-references: EMBL:X75761; NID:g415984; PID:g415985
C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-211 <RES>
A;Cross-references: EMBL:X14035; NID:943055; PID:943056
                                                                                                                                 DB 2;
                                                                                                                            Query Match 47.7%; Score 515.5; DB 2 Best Local Similarity 52.5%; Pred. No. 1.3e-40; Matches 106; Conservative 33; Mismatches 60
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F;25-46/Region: helix-turn-helix #status predicted
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1 ge 12-Jun	R.Waters, Superson A03574 R.Waters, Superson A03574 Nucleic Acids Res. 11, 6089-6105, 1983 A.Title: The tetracycline resistance determinants of RP1 and Tn1721: nucle A: Accession: A03574 A: Molecule type: DNA A: Residence number: A03574 A: Molecule type: DNA A: Residence: 1.216 (KMI)	C.Genetics: C.Genetics: A.Gene: tetR A.Gene: plasmid C.Superfamily: tetracycline repressor C.Keywords: antibiotic resistance; DNA binding; transcription regulation F;25-46/Region: hellx-turn-hellx #status predicted	216; 3; DALAIEN 1111	Qy 61 DRHHTHFCPLEGESWQDFIRNKAKSFRCALLSHRDGAKVHLGTRFTEKQYETLENOLAFL 12 S 1 1 1 1 1 1 1 1 1 1	C7 179 HOGENEPALFIGELIICGLEKQ 200 C7 179 HOGENEPALFIGELIICGLEKQ 200 C7 179 HOGENEPALFIGELIICGLEKQ 200 C7 180 EAGPDAAFEGGLAVITOGLII.	RESULT 10 H70740 Lypothetical protein Rv1353c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998 C;Accession: H70740 R;Cole, S,T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor: Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holro Nature 393, 537-544, 1998	A:Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Os; .; Taylor, K.; Whitehead, S.; Barrell, B.G. A:Title: Deciphering the biology of Mycobacterium tuberculosis from the A:Reference number: A70500: MUID:98295987 A:Accession: H70740	A) Modecule type: DNA A) Modecule type: DNA A) Residues: 1-261 <col/> A) Testidues: 1-261 <col/> A) Testidues: 1-261 <col/> A) Testidues: 1-261 <col/> A) Cross-references: GB:27555; GB:AL123456; NID:93261608; PID:e250355; IS, Experimental source: strain H37Rv C) Genetics: A) Genetics: A) GB:A	Ouery Match Best Local Similarity 28.1%; Score 176.5; DB 2; Length 261; Best Local Similarity 28.1%; Pred. No. 3.7e-09; Matches 61; Conservative 31; Mismatches 88; Indels 37; Gag QY 4 LDKSKVINSALELLNEVGIEGLITRKLAQKLGVEOPTLYWHVKNRRALLDALAIEMLDRH (::: : - : : : : : : : : : : : : : :

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R; Kunst, F; Gasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber R; Kunst, F; Gasawara, N; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; C.; Brow. S.; Broutllet, S.; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; C.; Brow. S.; Broutllet, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A; Authors: Fritz, C.; Frijita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Gh A; Authors: Fritz, C.; Frijita, M.; Kuita, K.; Lapidus, M.F.; Itaya, M. Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Laube Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Jardinois, S.; Laube A; Authors: Lazarevic, V.; Levine, A.; Sadale, Y.; Sato, T.; Scanlon, E.; Schl Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schl Rivolta, C.; Roche, E.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schl Mauchors: Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Gerol, S.J.; Ser A; Authors: Zumstein, E.; Yoshikaw, J.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vanden amakoshi, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshida, A; Reference number: A6580; MUID:98044033
A; Reference number: A69580; MUID:98044033
                                                                                                                                             Cispedies: Neisseria gonorrhoeae
A;Variety: strain FA19
C;Species: Neisseria gonorrhoeae
A;Variety: strain FA19
C;Date: 07-May-1908 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Date: 07-May-1908 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Date: No. Spratt, B.G.
Mol. Mcrobiol. 11, 769-775, 1994
A;Title: Regulation of the permeability of the gonococcal cell envelope by the mtr sy A;Reference number: $42417
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
C;Accession: H70042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 EH--TEQNA--AVIAIA------RKHQAIWREKIT-----AVLTEAVENQDLAD 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z25797; NID:g452332; PID:g438189
A;Experimental source: strain FA19
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   155 DDLDKETAVIF 165
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A; Residues: 1-210 <PAN>
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Myl. Microbiol. 11, 769-775, 1994
A;Title: Regulation of the permeability of the gonococcal cell envelope by the mtr syste
A;Reference number: S42417
A;Reference number: A69580; MUID:98044033
A;Accession: A69900
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A;Residues: 1-191 <KUN>
A;Residues: 1-191 <KUN>
A;Residues: 1-191 <KUN>
C;Genetics: GB:Z99114; GB:AL009126; NID:92634230; PID:e1185379; PID:92634300
C;Genetics:
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A;Variety: strain CH95
C:Date: O'N May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C:Accession: S42417; S40251
R:Pan, W.; Spratt, B.G.___
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LDRHHTHFCPLEGES------WQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 FDQMADSVIERKGDSAMLSLAHAYVDFAIENPGYYEAALL-----KVH-----DKRTE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 119; DB 2; Length 191;
23.6%; Pred. No. 0.00051;
tive 39; Mismatches 74; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LIQKMIVDAAAEIADQEGVNGVSLAALSKKMNVRPPSLYNHINGLQAIRAELAVRGLIKL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%; Score 110.5; DB 2; Length 210; Best Local Similarity 27.2%; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL: Z25796; NID: 9438190; PID: 9438191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
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S.superfamily, probable transcription repressor mtrr
C;Reywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 FSIR------TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 DHQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-210 <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S42417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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Best Local S
                                                                                                                                                                                                                                                                                                                     A; Gene: yobs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

Indels 43;

-----NILFLKC 116

A:Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PID:e1184426; PID:g2636046 A:Experimental source: strain 168 C:Genetics: A:Gene: yvkB

Search completed: June 9, 1999, 12:59:50 Job time: 9169 sec

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OM protein - protein search, using sw model

June 9, 1999, 10:29:01; Search time 16.52 Seconds (without alignments) 336.316 Million cell updates/sec

Run on:

US-08-486-814-17 1080

1 MSRLDKSKVINSALELLNEV.. Perfect score: Sequence:

......FGLELIICGLEKQLKCESGS 207

74019 seqs, 26840295 residues Searched:

BLOSUM62

Scoring table:

SwissProt_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scription	scherichi	P51562 pasteurella	escherichi	a,	(1)	escheri	escheri	vibrio ang	Q11023 mycobacteri	P39897 neisseria g	059431 escherichia	mus muscul	P75952 escherichia	P23217 staphylococ		azotobac		escherich		Q09684 schizosacch	P12263 sus scrofa	escherich									S	P31676 escherichia	Pl1501 gallus gall	P33176 homo sapien	schizosacc			drosophil	homo	သ	saccharomy	mus muscul	esc
SUMMA	TER2 ECOLI			TER8_PASMU	- 1	TER1_ECOLI	TER5_ECOLI	TER7_VIBAN	YO7H_MYCTU	MTRR_NEIGO	UIDR_ECOLI	SKD3_MOUSE	YCFQ_ECOLI	YP23_STAAU	BETI_ECOLI	NIFL_AZOVI	PHSL_IPOBA	YFAX_ECOLI	YWFK_BACSU	THT1_SCHPO	FA8_PIG	TTK_ECOLI	BM3R_BACME	MYSP_SCHJA	VACB_HAEIN	ACRR_ECOLI	SPCN_HUMAN	TRC5_ECOLI	YCDC_ECOLI	FA8_MOUSE	YD86_SCHPO	ENVR_ECOLI	HS9A_CHICK	KINH_HUMAN	YDH6_SCHPO	TTK_HAEIN	Y893_HAEIN	CF1A_DROME	HS9B_HUMAN	MY SP_SCHMA	N157_YEAST	UFO MOUSE	ECO
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P12758 escherichia P16749 human cytom
UDP_ECOLI IE63_HCMVA
252
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74.5
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ALIGNMENTS

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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89094871.

MEDLINE; 89094871.

J. MOL. BIOL. 203:949-959(1988).

ELEMENT: ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.

J. SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T->I: REDUCES AFFINITY FOR TETRACYCLINE LESS THAN 10 FOLD.
4AB4DD5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H->Y: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N->H: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
99.5%; Score 1075; DB 1; Length 207;
Best Local Similarity 99.5%; Pred. No. 5.6e-93;
Matches 206; Conservative 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGNESIUM (OF [MG-TC]+ COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X00694; G43052; -.
EMBL, J01830; G154846; -.
PIR, A03576; RPECTN.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; TRANSPOSABLE ELEMENT;
DNA-BINDING; ANTIBIOTIC RESISTANCE.
DNA_BIND
26 45 H-T-H MOTIF (POTENTIAL).
                                                                         01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON TNIO).
                                                                                                                                                                                                                                                                BERTRAND K.P., POSTLE K., WRAY L.V. JR., REZNIKOFF W.S.; GENE 23:149-156(1983).
                     207 AA
                                                             LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1000 FOLD.
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE, 84247342.
MEDLIEK, NGUYEN T.T., BERTRAND K.P.;
PUCLEIC ACIDS RES. 12:4849-4863(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 FOLD
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
                                               13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQI
01-OCT-1996 (REL. 34, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA; 23354
                                                                                                                                                                                                                                         SEQUENCE OF 1-22 FROM N.A.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
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                                                                                                                                               ENTEROBACTERIACEAE
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                                                                                                                    ESCHERICHIA COLI
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        TER2_ECOLI
ID TER2_ECOLI
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                                                                                                                                                                                                                                                         MEDLINE;
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                                     P04483
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PASTEURELLACEAE.
121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                  MICROBIOL. IMMUNOL. 38:31-38(1994).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELIX-TURN-HELLX STRUCTURE. AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE] COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETRACYCLINE OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |||| : ||||| ||| ||| || || || :|
121 TENGFSLRDGLYAISAVSHFTLGAVLEQOEHTAALTDRPAAPDENLPPLLREALQIMDSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
3C57D4AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%; Score 683; DB 1; Length 218; 65.2%; Pred. No. 1.5e-56; Live 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D16172; G575938; -
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
                                                                                                                                                                                         01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                                                                      218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                           181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                             181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 DGEQAFLHGLESLIRGFEVQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TER4_ECOLI STANDARD;
P09164;
01-MAR-1989 (REL. 10, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                   PASTEURELLA PISCICIDA. PLASMID PSP9351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94328963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                   TER8_PASPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                  TER8_PASPI
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GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                   62 RHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQG 181
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                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                 MEDLINE; 94204640.
HINRICHS W., KISKER C., DUEVEL C., MUELLER A., TOVAR K., HILLEN W.
                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES-S.ORDONEZ; STRAIN-BM2000; PLASMID-PIP173;
MEDLINE; 93204906.
ALLARD J.D., GIBSON M.L., VU L.H., NGUYEN T.T., BERTRAND K.P.;
MOL. GEN. GENET. 237:301-305(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+.
830EFSEB CRC12;
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.8%; Score 678; DB 1; Length 217; 65.0%; Pred. No. 4.4e-56; Live 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB: ZTCT; 03-DER-96.
PROSITE; 20-JUN-96.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTIBIOTIC RESISTANCE; 3D-STRUCTURE.
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS D.
                                                                                                                SEQUENCE FROM N.A.
SPECIES-E.COLI; STRAIN=J53-1; PLASMID-RA1;
MEDLINE; 85037938.
                                                  ESCHERICHIA COLI, AND SALMONELLA ORDONEZ.
                                                                                                                                                     UNGER B., KLOCK G., HILLEN W.;
NUCLEIC ACIDS RES. 12:7693-7703(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 II
99 MA
24287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||| ||| :| | ||
181 GEQAFLHGLESLIRGFEVQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X01083; G43054; --
EMBL; X65876; G49075; --
PIR; S07359; S07359,
PIR; S30287; S30287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                         ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATORS.
                                                              PLASMID PIP17
PROKARYOTA; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID PVM111.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM--PPLLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                      ANTIMICROB. AGENTS CHEMOTHER. 37:2699-2705(1993).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO-TEMINAL REGION FORMS A HELIX-TURN-HELIX STRUCTURE AND BINDS DAR. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE ESISTANCE GENE
                                                                                                                                                                                                                                                                                                        (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 673; DB 1; Length 207; 64.2%; Pred. No. 1.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                 EMBL, U00792; G392872; -.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45 H-T-H MOTIF (POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A51DA28B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS C.
                                                 (REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Pred. No. +ive 27; Mismatches
          207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                               TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 HQGAEPAFLFGLELIICGLEKQLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 SDNGDAAFLFVLDVMISGLETVLK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
                                      01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA; 23156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                             PASTEURELLA MULTOCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCHERICHIA COLI.
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                 STRAIN-P2862;
MEDLINE; 94153051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                     PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                          REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TER3_ECOLI P03039;
                                                    01-0CT-1996
                                                                 01-OCT-1996
             PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                         P51561
TER8_PASMU
                                                                                                 TETR.
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PLASMID RP1, AND PLASMID RP4.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOL. BIOL. EVOL. 2:1-12(1985).

-1- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
-1- FUNCTION: TIS AMINO-TEMINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DAR. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                   1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                  (TETA) PROMOTER OPERATOR SITES.
                                                                                                                                                                                                                  INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                                                                                                                                                MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                               48.6%; Score 525; DB 1; Length 219; 52.7%; Pred. No. 7.2e-42; tive 32; Mismatches 60; Indels
                                                                                                                                                                    PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTBIOTIC RESISTANCE.
DNA_BIND 6 45
H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS A (TRANSPOSON 1721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRUEMAN P., SHARPE G.S., BARTH P.T.;
SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B., GRECK M., SCHMITT R.;
                                                                                                                                                                                                                                                                            6C9E1828 CRC32;
                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                            219 AA; 24174 MW;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                           EMBL; M36272; G150946; -. PIR; A03575; RPECYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                            45
64
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GENE 111:11-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID=PLASMID RP4;
                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSPOSON=TN1721;
MEDLINE; 92192465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
             MEDLINE; 88216101
                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                          64
                                                                                                                                REGULATORS.
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                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
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TER1_ECOLI
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SEQUENCE FROM N.A. TRANSPOSON-TN1721; PLASMID-RP1; MEDLINE; 83299270.

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WATERS S.H., ROGOWSKY P., GRINSTED J., ALTENBUCHNER J., SCHMITT R.;
NUCLEC ACIDS RES. 11:6089-6105(1983).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT, ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOVAR K., ERNST A., HILLEN W.;

MOL. GEN. GENET. 215:76-80(1988).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT, ITS AMINO-TERMINAL REGION FORMS A HELIX-TUBN-HELIX
STRUCTURE AND BINDS DAY. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
(TETA) PROMOTER OPERATOR SITES.

-!- SIMILARITY: BELONGS TO THE TETRACARR FAMILY OF TRANSCRIPTIONAL
                                                                                             (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                  INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 515.5; DB 1; Length 216; 52.5%; Pred. No. 5.4e-41; tive 33; Mismatches 60; Indels 3
                                                                                                                                                                                                                                                                                                                                     MAGNESIUM (OF [MG-TC]+ COMPLEX)
                                                                                                                                                                                                             TH -> ST (IN REF. 3).
I -> T (IN REF. 3).
DA -> ES (IN REF. 3).
F72BDFB1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 AA.
                                                                                                                                                                                                                                                                                  H-T-H MOTIF
                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 HQGAEPAFLFGLELIICGLEKQ 200
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180 EAGPDAAFEQGLAVIVDGLAKR 201
                                                                                                                                                                                                                                                                                                                                                               66 TF
80 I
155 DZ
23320 MW;
                                                                                                                                                         EMBL; X61367; G48198; -
EMBL; X75761; G415985; -
EMBL; X00006; G42509; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                              80
154
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89201249
                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                  REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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ID TER5_EC

AC P21337

DT 01-MAY.

DT 01-MAY.

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PROKARYOTA; GRACILLICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
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INVOLVED IN BINDING TO [MG-TC]+ (BY
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EMBL; X14035; G43056; --
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.2%; Score 509.5; DB 1; Best Local Similarity 51.2%; Pred. No. 1.9e-40; Matches 103; Conservative 29; Mismatches 66;
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F538C813 CRC32;
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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23585 MW;
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                                                                                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                        1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WURBHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL.
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
16.3%; Score 176.5; DB 1; Length 261;
Best Local Similarity 28.1%; Pred. No. 2.1e-09;
Matches 61; Conservative 31; Mismatches 88; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 275555; E250355; -.
PROSITE; PS01081; HTH_TETR_EAMILY; FALSE_NEG.
PROSITE: PS01081; HTH_TETR_EAMILY; FALSE_NEG.
PROPHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.
BNA_BIND
DNA_BIND
SEQUENCE 261 AA; 28253 MW; 8CBBCC98 CRC32;
                                                            / Match
Local Similarity 48.8%; Pred. No. 2.3e-38;
Los 98; Conservative 29; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      011023;
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNORATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR CY02B10.17C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 TPTTDSMPPLLRQAIELFDHQGA--EPAFLFGLELII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 HQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : || |||: :| ||:
181 TDGMDAAFNFGLDSLIAGFER 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYCOBACTERIUM TUBERCULOSIS
                                                                                                                        98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X07H_MYCTU
ID Y07H_MYCTU
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
MTRR_NEIGO
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
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210 AA.

PRT;

STANDARD;

MTRR_NEIGO P39897;

a S

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SEQUENCE FROM N.A.
STRAIN=KIZ / MAG1655.
STRAINERIZ / GA1655.
BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FA19;
MEDLINE; 9424732.
MEDLINE; 9424732.
PAN W., SPRAT B.G.;
MOL. MICROBIOL. 11:769-775(1994).
-!- FUNCTION: PUTATIVE REPRESSOR OF WIRC GENE. CONTROLS THE PERMEABLILITY OF THE CELL ENVELOPE TO HYDROPHOBIC COMPOUNDS SUCH AS ANTIBIOTICS AND DETERGENTS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z23727, Z40250. S40250. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 CIAQDAADAEGGSWIVF-RHILLHFFERLQSNDIHYKFH-------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 EH--TEQNA--AVIAIA------RKHQAIWREKIT-----AVLTEAVENQDLAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ----HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEISSERIA GONORRHOEAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 27.4%; Pred. No. 0.0021;
Matches 52; Conservative 22; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON K.J., JEFFERSON R.A.;
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UID OPERON REPRESSOR (GUS OPERON REPRESSOR).
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z25797; G438189; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                     REGULATORY PROTEIN MIRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 HQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 DLDKETAVIF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULATORS.
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SCUENCE FROM N.A.
STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                     96 GAKVHLGTRPTEKQYE-TLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQE-HQV 153
                                                                                                                           582 GYNVHYGARSIKHEVERRVVNQLAAAYEQDL-----LPGGCTLRITVEDSDKHLL 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 DRDAALDKAMKLFWQHGYEATSLADLVEATGAKAPTLYAEFTNKEGLFRAVLDRYIDRFA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 AKHEAQLFCEEKSVESALADYFAAIANCFTSKDTPAGCFMINNCTTLSPDSGDIANTLKS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 --HHTH-FCPLEG--ESWQDFLRNKAKSF-------RCALLSHRDGAKVHLGTR 104
                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN NDH-MFD INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 DKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION (ORF 188).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 85.5; DB 1; Length 236; Best Local Similarity 24.5%; Pred. No. 0.52; Matches 34; Conservative 17; Mismatches 65; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOGENE; EG13435; YCFO.
PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG.
HYPOTHETICAL PROFEIN; TRANSCRIPTION REGULATION; REPRESSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 91211614.
REQUEN D.A. CRAM D.S., DIBERARDINO D., LITTLEJOHN T.G.,
SKURRAY R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 86 H-T-H MOTIF (POTENTIAL).
236 AA; 26204 MW; AD1F64FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE
                                                                                                                                                                                                                                                                                                                                           236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                            154 AKEERETPITDSMPPLLRQAIELFD 178
                                                                                                                                                                                                                632 KSPELPSPQAEKRPPTLR--LEIID 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (REL. 20, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G1787354; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 PTEKQYETLENQLAFLCQQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 RHAMOERTLQO---FLCOR 181
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAPHYLOCOCCUS AUREUS.
PLASMID PSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000211:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-BINDING.
                                                                                                                                                                                                                                                                                                                             YCFQ_ECOLI
P75952:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YP23_STAAU
P23217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                             YCFQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
YP23_STAAU
                                                                                    δŽ
                                                                                                                              g
                                                                                                                                                                          δ
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              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERIER F., RADEKE C.M., RAAB-GRAHAM K.F., VANDENBERG C.A.; GENE 152:157-163(1995).
-!- TISSUE SPECIFICITY: PRESENT IN A WIDE VARIETY OF TISSUES, IS ABUNDANT IN MOUSE HEART, SKELETAL MUSCLE AND KIDNEY, AND IS MOST ABUNDANT IN TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLG--------VEQPTLYWH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 VKNKRAL--LDALAIEMLDRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHR-----D 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
-!- SIMILARITY: HIGH, TO OTHER MEMBERS OF THE CLPA/CLPB FAMILY.
MGD; MGI:1100517; SKD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 95.5; DB 1; Length 196; 25.3%; Pred. No. 0.049; tive 23; Mismatches 32; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 85.5; DB 1; Length 677; 22.4%; Pred. No. 1.8; tive 32; Mismatches 84; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                   H-T-H MOTIF (POTENTIAL).
: 6C1840FC CRC32;
                                                                                                                                                                                                                                     EMBL; M14641; G868019; --
EMBL; M14641; G1787904; --
EMBL; D90805; G1742672; --
ECOGENE; EG1267; UIDR.
PROSITE: F991081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION_REGULATION; DNA-BINDING; REPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 358 ATP (POTENTIAL).
677 AA; 76003 MW; FF6EF81E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-BINDING; REPEAT; ANK REPEAT.
NP_BIND 351 358 ATP
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 196 AA; 21799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | |:|| : |::
73 RFREPIEGIHFVDYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKD3 PROTEIN.
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SEQUENCE
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STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AE000138; G1766505; -.
EMBL: AE000138; G1765505; -.
EMBL: 073867; G1657511; ALT_INIT.
PIR: $10899; $10899;
PIR: $15180; $15180.
EXCOGENE; EG10111; BETI.
PROSITE; PS01081; HTH_FETR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR; TRANS-ACTING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLCQQGF 125
                                                                                                                                      EMBL; X56628; G46660; -.
PIR; S12393; S12393.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING; PLASMID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||: : | : : : | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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DUNCAN M., ALLEN E., ARAUJO R., APARICIO A.M., CHUNG E., DAVIS K.,
FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H.,
LIN D., NAMATH A., OEFNER P., ROBERED D., SCHRAMM S., DAVIS R.W.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-i - FUNCTION: REPRESSOR INVOLVED IN CHOLINE REGULATION OF THE BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- PATHWAY: OSMOREGULATORY CHOLINE-GLYCINE BETAINE PATHWAY.
-i- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
MOL. MICROBIOL. 4:2051-2062(1990).
-!- FUNCTION: POSSIBLE TRANSCRIPTIONAL REPRESSOR OF THE QACA GENE.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92065800.
LAMARK I., KAASEN E., ESHOO M.W., FALKENBERG P., MCDOUGALL J.,
STROM A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 7.8%; Score 84; DB 1; Length 188; Best Local Similarity 22.2%; Pred. No. 0.54; Matches 28; Conservative 25; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                 24 43 H-T-H MOTIF (POTENTIAL).
188 AA; 22174 MW; D4A58A93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 AA.
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                                                                                                          REGULATORS.
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                                                                                                                                                                                                                                                                            REPRESSOR.
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SEQUENCE
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BETI_ECOLI
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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June 9, 1999, 10:28:01; Search time 28.57 Seconds (without alignments) 399.721 Million cell updates/sec US-08-486-814-17 1080 1 MSRLDKSKVINSALELLNEV.....FGLELIICGLEKQLKCESGS 207 OM protein - protein search, using sw model **BLOSUM62** Title: Perfect score: Sequence: kun on:

180763 seqs, 55169189 residues Scoring table:

Searched:

sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_archea:* sp_fungi:*
sp_human:*
sp_human:*
sp_novertebrate:*
sp_mammal:*
sp_nnc:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_bacteria:*
sp_rodent:* SPTREMBL_8:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ď			SUMMARIES		Z C
Result		Query					DR
No.	Score	Match	Match Length DB	DB	ΠD	Description	N N
г	619	57.3		6	059466	Q59466 haemophilus	KW
7	149.5	13.8		6	Q53901		os
٣	129.5	12.0		6	052558		
4	119	11.0		σ	034892		
Ŋ	110.5	10.2		σ	Q59608		_
ø	108.5	10.0		σ	034643		ш
7	101.5	4.6	192	σ	067927		2.
œ	86	9.1		σ	053789		
σ	94.5	8.8		6	Q51597		οy
10	94.5	8.8		σ	P73186		
11	94	8.7		0	067157	067157 aquifex aeo	qq
12	94	8.7		σ	087854		
13	93.5	8.7		6	053295		οy
14	92	8.5		6	053310		
15	83	8.2		σ	007001		ପ୍
16	88.5	8.3		6	070020		
17	87.5	8.1		6	025951	025951 helicobacte	δλ
18	86.5	8.0		14	029994	O29994 archaeoglob	
19	86	8.0		6	051516	Q51516 pseudomonas	<u>අ</u> ධ
20	85	7.9		6	051730	Q51730 pseudomonas	
21	85	7.9		6	P96676	P96676 bacillus su	
22	84.5	7.8	7	10	P70477	P70477 rattus norv	RES
23	84.5	7.8		10		O88663 rattus norv	02
24	84	7.8		σ	034970	034970 bacillus su	Ω -
25	84	7.8		σ		Q59802 staphylococ	AC
26	ຕ	7.7	435	7	_	075901 homo sapien	DI
27	83.5	7.7		σ	P95100	P95100 mycobacteri	DT
78	83.5	7.7		17	091290	Q91290 pleurodeles	DI
29	83	7.7		ო	018399	018399 drosophila	DE

Q42863 ipomoea bat O67930 aquifex aeo Q06919 azotobacter	Q13186 homo sapien O59147 pyrococcus O75181 homo sapien Q54830 streptococc	008961 rattus norv 008961 rattus norv 019126 macaca fasc 019127 macaca mula	00038 Nome Saptem 014812 home saptem 053165 mycobacteri 059306 clostridium 007388 mycobacteri
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		581 1186 285 285	2442 1842 180 190
7.7	9.777	2.7.7.7.	44444
888	82.5 82.8 81.5 81	81 80.5 80.5	00000
30 31 32		37 38 39 40	44444 10642

ALIGNMENTS

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AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 LAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEE-------RET 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 MNLLRSGGLHDELAAYGGDLLSTFVTAEALEQSSRNPGTEQGREQAGVFADQLHGYLKSL 202
                                                                                                                                                                                                                                                                                                  37; Gaps
                                                                                                                                                                                                                                                                                                                         4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDAL----AI 57
                                                                                                                                                                                                                                                                                                                                                      31 LTQDRIVVTALGILDAEGLDALSMRRLAQELKTGHASLYAHVGNRDELLDLVFDIVLTEV 90
                                                                                     MEDLINE; 91347376.
FERNANDEZ-MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F.; FERNANDEZ-MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F.; dire act cluster contains regulatory and antibiotic export genes, direct targets for translational control by the bida tRNA gene of Streptomyces.", Streptomyces.", Streptomyces.", ENBL, M64683; G455360; PENBL, M64683; G455360; PENBL, M64683; G455360; SEQUENCE 259 AA; 28268 MW; 16ECA071 CRC32;
                                                                                                                                                                                                                                                                13.8%; Score 149.5; DB 9; Length 259; 26.0%; Pred. No. 4.5e-06; Live 35; Mismatches 90; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W.,
TATLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; FIRMICUTES; ACTINOBACTERIA; PSEUDONOCARDIACEAE;
                              BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G.;
J. BIOL. CHEM. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 PTTDSMPPLLRQA--IELFDHQGAEPAFLFGLELIICGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 PAT-SFPNLVHLAGPITSLD---SDRRFELGLEIIIAGL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF040570; G2792330; -. SEQUENCE 242 AA; 27049 MW; 324EB570 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMYCOLATOPSIS MEDITERRANEI
                                                                                                                                                                                                                                                                                             57; Conservative
            STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 57; Conserva
                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052558;
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12.0%; Score 129.5; DB 9; Length 242;

Query Match

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RA MENDINE; 9404403.

RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,

RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,

RA BOULLET S., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,

RA CHOI S.K., CODANI J.J., CALDWELL B., CAPDANO V., CARTER N.M.,

RA CHOI S.K., CODANI J.J., CALDWELL B., CADMINGS N.J., DANIEL R.A.,

BRUILDTA K., FULITA Y., FUNAS K., GALIZI A., GALIZIA P., COULGEP D., FRITZ C.,

RA GLASAPEL S., HAGA K., HAIECH Y., FARRET C., FERRAIL S., FOULGEP D., FRITZ C.,

RA GLASAPEL S., HAGA K., HAIECH J., HARWOD C.R., HENAUT A., HILBERT H.,

RACHER P., COFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G.,

RACHINGS S., LACHER J., HAGA K., HAIECH J., HARWOD C.R., HENAUT A., ILLEET H.,

RACHINGS S., LACHER J., HAGA K., HOLLO M.F., ITAYA M., JONES L., JORIS B.,

RARAMARA D., KASHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y.,

RACHINGS S., LACHER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H.,

MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,

MOESTL D., NAKAI S., NOBAKO, M., NOONE D., O'REILLY M., PORPETELLE D.,

RA PORWOLLIK S., PRESCOTT A.M., PRESECAN E., FORDINA C., ROCHA E.,

RA ROCHE B., ROSE M., SADAIE Y., SEKIGICHI J., SEKOWSKA A., TAKAGI T.,

RA SCHROETER R., SCOFFONE F., SEKIGICHI J., SEKOWSKA A., TAKAGI T.,

RA SERNO R., SHIN B.S., SOLLO B., SOROKIN A., TACCONI E., TAKAGI T.,

RA VANIBR R., VASSAROTI A., VIARI A., WAMBUTT R., WEDLER E., WEDLER E.,

VANIBR R., VASSAROTI A., VIARI A., WAMBUTT R., WEDLER E., WEDLER E.,

RASUMOTO K., YATA K., YORATO V., VOHINAMA H.F., ZUMSTEIN E.,

RA SUNOTO K., YATA K., YORATO V., YORHIKAMA H.F., ZUMSTEIN E.,

RA PORMOLLINE R., WINTERS P., WIRAI A., YAMAMOTO H., YAMANE K.,

RA SUNOTO K., YATA K., YORATO A., YOSHIKAMA H.F., ZUMSTEIN E.,

RASUMOTO K., YATA K., YOSHIDA K., YOSHIKAMA H.F., ZUMSTEIN E.,

RACHER COMPLETION A., YATA K., YOSHIKAMA H.F., ZUMSTEIN E.,

RACHER C., WINTER P., WINTERS P., WIRAI A., YAMAMOTO W., YOSHIKAMA H., PONELL W., YOSHIKAMA H., DANCHIN A., YOSHINA K., YOSHIKAMA H., PONEL 
                                                                                                                                                           EM----LDRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKV---HLGTRPTEKQY 110
                                                                                                                                                                                         111 ETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ----EHQV----AKEERETPTT 163
                                                                                                                                                                                                                                                                                 | | : | : | : | : | : | 138 --TECAQAVAACSPLPLKDRSAALNVVFQYVXGFTATESRWLEHLAETGRTAEEFAAEVT 195
                                29; Gaps
                                                                                                  2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRAL----LDALAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
       26.2%; Pred. No. 0.00025;
tive 35; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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05,
08,
Best Local Similarity 26.2 Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           164 DSM 166
                                                                                                                                                                                                                                                                                                                                                                                      196 GSM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
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034892
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3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
178 DHQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                  KARAMATA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 CIAQDAADAEGGSW-----TVFRHTLL-----HFFERLQSNDIYYKFHNILFLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                         60 LDRHHTHFCPLEGES------WODFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                  74; Indels 42; Gaps
                                                                                                                                                                                                                                                                        4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
10.2%; Score 110.5; DB 9; Length 210;
Best Local Similarity 27.2%; Pred. No. 0.011;
Matches 52; Conservative 21; Mismatches 73; Indels 45
                                                                                                                                                                                       Ouery Match 11.0%; Score 119; DB 9; Length 191; Best Local Similarity 23.6%; Pred. No. 0.0016;
                     KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.; SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF027868; G2619045; -. EMBL; 299114; E1185379; -. SEQUENCE 191 Aa; 21016 MW; CB192356 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 AA; 24218 MW; E2FEDFC3 CRC32;
                                                                                                                                                                                                                                   39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z25796; G438191; -.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
PFAM; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 FSIR-----TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30S RIBOSOMAL PROTEIN S21.
                                                                                                                                                                                                                                     48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEISSERIA GONORRHOEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIBOSOMAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
01-NOV-1998
          STRAIN-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   059608;
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RA MUSTER, SOURGERER, MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZUNGO, V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZUNGO, V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRISS R., BOURSIER I., BRANG A., BRAUM W., BRIGHELL S.C., EARTER N.M.,
RA GUILLET S. W., CODANI J.J., CONNERTON I.F., CALDANO V., VARAMO V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOSHIKAWA H., DANCHIN A.; "The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
LAZAREVIC V., SOLDO B., RIVOLTA C., REYNOLDS S., MAUEL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF011113; G2618838; -.
EMBL; Z99122; E1184426; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 19.6%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 390:249-256(1997).
                                                                                                                                                                                                                              PRELIMINARY;
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155 DDLDKETAVIF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Query Match
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Matches 4
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                                                                                                                                       123 QGFSLENALYALSAVGHFTLGCVLEDQEHQ------VAKEERETPTTDSM 166
                                                                                                                                                                      STRAIN=VF5;
MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RHHTHFCPLEGESWQDFLR-----NKAKSFRCALLSHRDGAKVHLGTRPTEKQY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 RHKLEVALQRGETDEBILLESIVDTLIDYAFSNPESFRFLNLXH------LLKEY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ETLENQ-----LAFICQOGFSLENALY---ALSAVGHFTLGCVLEDQEHQVAKEER---- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GEVKNLPGELILKFL-----NGLYLKRKLKTYPEIALAVVTGSVERVFIFKERNFLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYMHVKNK----RALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
9.4%; Score 101.5; DB 9; Length 192;
Best Local Similarity 22.7%; Pred. No. 0.06;
Matches 45; Conservative 34; Mismatches 68; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                01-505-1998 (TREMBLREL. 07, CREATED)
01-505-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
                                                                                                                                                                                                                                                                                                                                                                         192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 AA.
                                                                                                                                                                                                                     167 PPLLRQAIELFDHQG-----AEPAFLF 188
                                                                                                                                                                                                                                                           120 KOLLVDYLKTMGEKGVIQTGNEAEHADVF 148
                                                                                                   62 RGSILEQTEGDLYKDLL------
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 -- ETPTTDSMPPLLRQAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 YDEETIKKELKKVLKSAI 190
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQUIFEX AEOLICUS.
                                                                                                                                                                                 83 ---
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053789
ID 053789
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
MYCOBACTERIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 DIITMLNRVGAGRARDDAVLVWAGAYR-SYAHHHPGRYSAFTRMPLGGDDPEYTAATRGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHYKNKRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86223770.
KOGA H., ARAMAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T.,
GUNSALUS I.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "camR, a negative regulator locus of the cytochrome P-450cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch
1 Similarity 27.3%; Pred. No. 0.13;
42; Conservative 24; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                               HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; AL021943; E1253107; -.
SEQUENCE 196 AA; 21262 MW; 17D86001 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 LENQLAFLCQQGFSLENALYAL----SAVGHFTL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AAPVIAVLSSYGLDGEQAFYAALEFWSALHGFVL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AA
                  CREATED)
01-JUN-1998 (TREMBLREL. 06, CREATED. 01-JUN-1998 (TREMBLREL. 06, LAST SEC 01-NOV-1998 (TREMBLREL. 08, LAST AN) PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydroxylase operon.";
J. BACTERIOL. 166:1089-1095(1986).
                                                                                                                                 MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96181548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAM REPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEUDOMONAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLE S.T.;
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PRELIMINARY;
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                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98196666.
                                                                                                                                                                                                                                                                                                AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                                                       STRAIN=VF5
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYALIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                   ARAWAKI H., SAGARA Y., TAKEUCHI K., KOGA H., HORIUCHI T.; "Nucleotide sequence of the gene encoding a repressor for the cytochrome P-450cam hydroxylase operon on the Pseudomonas putida CAM
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                    6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKN----KRALLDALAIEMLD 61
                                               ARAMAKI H., KOGA H., SACARA Y., HOSOI M., HORIUCHI T.; "Complete nucleotide sequence of the 5-exo-hydroxycamphor dehydrogenase gene on the CAM plasmid of Pseudomonas putida (ATCC
                                                                                                                                                                                                                                                                                                                                           .
6
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8.8%; Score 94.5; DB 9; Length 236;
Best Local Similarity 22.5%; Pred. No. 0.33;
Matches 36; Conservative 24; Mismatches 55; Indels 4.
                                                                                                                                                                                                                                                                                                                  Length 186;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 26.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                               8.8%; Score 94.5; DB 9;
28.6%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA; 26384 MW; A8D84E37 CRC32;
                                                                                                                                                                                                                                                                          186 AA; 20438 MW; 56E43196 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA.
                                                                                                                                                                                                                                                                                                                                           20; Mismatches
                                                                                                     BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90904; G1652289; -.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
PFAM; PF00440; LetR; 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TREMBLREL: 02, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STRAIN PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                          62 RHH---THFCPLEG--ESWQDFLR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AYHGGTEERGPLKGIRDGWATFLQ 87
                                                                                                                                                                                                                                                                                                                  8.8%
Ouery Match
Best Local Similarity 28.6%
Matches 24; Conservative
                                                                                                                                                                                                                    BIOCHIMIE 76:63-70(1994).
EMBL; D14680; G473745; -.
PFAM; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA RES. 3:109-136(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                               SEQUENCE FROM N.A.
[2]
SEQUENCE FROM N.A.
                                    MEDLINE; 93326643.
                                                                                                                                                       MEDLINE; 94304997
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                                                                                                                                              STRAIN-PPG
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                           plasmid.
                                                                                                                                                                                                                                                                PLASMID.
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97 DLLCSEKFRNIYFEKIEDAKRRFEKFLEKHFPSKAEILSEIILGFLRQLILHYVIKEERE 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETL--ENQLAF---- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KERILEVSKELFFEKGYOGISVEEIVRRANLSKGAFYFHFKSKEELI----TEIIERTHK 59
                                                                                                                                            68 CPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEK-QYETLENQLAFLCQQGFS 126
                                                                                                                                                                                                              96 ----AGWVEILTD-----RRMFH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                            46 RILKGALKLFGTKGYEGTTTKDLAQAANVAEGTLFRYFTNKKAILVEVAT----- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
ک
8 KVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 KIISL-----FEENKEKTPEELL-------EMFLEVLYREKKVVYIFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=VF5;

BECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
EMBL, ABOOO721; G298349; -.
SEMBL, ABOOO721; G298349; -.
SEMBL, ABOOO721; G298349; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 LP---FLKEKLRE-------GLKLIFEGVKK 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                        127 LENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM 166
                                                                                                                                                                                                                                                                                                                                                           129 LRENKYLLQV-----CFVEAQYHPELREKIQSEIIDKM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AA.
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01-NOV-1998 (TREMBLREL. 08, LAST SEQ
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ID 06
AC 06
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Gaps

55; Indels 45;

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STRAIN-H37RV;
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               leprae.";
                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN—A3(2);
MEDLINE; 97000351.
REDEMBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KIRASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. MICROBIOL. 21:77-96(1996).
EMBL, AL031013: E1309426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.7%; Score 94; DB 9; Length 217;
Best Local Similarity 34.1%; Pred. No. 0.33;
Matches 29; Conservative 14; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                           STREPPOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES;
STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                             SEGER K.J., HARRIS D.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                        PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37RV;
OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 AA
                    PUTATIVE TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 HHTHFCPLEGESWODFLRNKAKSFR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLEEL. 06, L
01-NOV-1998 (TREMBLEEL. 08, L
HYPOTHETICAL 27.6 KD PROTEIN.
MTV012.65C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                           STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
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053295
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                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | :| :: :| :: | 91 AIFPSIDLAIDSAREVIRRSVEEYVNLVDQHPNVLRVFIQGRSAKQSEATVRTLNEGREI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TLAMAEMFNNELREMELNRAALELAAFAAFGSAASATEWWLGPEPDSPRRMPREQFVAHL 210
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MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE; MYCOBACTERIAD.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                        6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                              32 RNEIVDAAFRAIDRLGPE-LSVRQIAEEAGTAKPKIYRHFTDKSDLLEAIGMRLRDMLWA 90
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BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                        Query Match 8.7%; Score 93.5; DB 9; Length 246; Best Local Similarity 19.0%; Pred. No. 0.42; Matches 41; Conservative 42; Mismatches 82; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.5%; Score 92; DB 9; Length 213;
Best Local Similarity 35.8%; Pred. No. 0.48;
Matches 24; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TREMBLREL. 06, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; AL021287; E1237796; -.
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EMBL; AL021646; E1248751; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 TEKQYETLENQLAFLCQQGFSLENALYAL-------
                                                                                       246 AA; 27618 MW; DC3E2076 CRC32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 TILMMGVIVGTAEALGIAVDPOQPIHDAVPNNPAVR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 T---LGCVLEDQEHQVAKEERETPTTDSMP--PLLR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 08, L. HYPOTHETICAL 23.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                               HYPOTHETICAL PROTEIN.
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RA AZEVEDO V. BERTERO M.G. BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V. BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORNISS R., BOURGIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUTLLET S., BRUSCHI C.V. CALDWELL B., CARDANO V., CARTER R.M.,
BROUTLLET S., BRUSCHI C.V., CALDWELL B., CARDANO V., CARTER R.M.,
BROUTLLAT S., BRUSCHI C.V., CALDWELL B., CARDANO V., CARTER R.M.,
BROTTAM M.D., ERRINGTON J., FABRET C., FERRALI E., FOULGER D., FRITZ C.
GLOSER P., GOFFEAN A., GOLIGHTIY E.J., GRANDI G., GUISEPPI G.,
RA GLASER P., GOFFEAN A., GOLIGHTIY E.J., GRANDI G., GUISEPPI G.,
RA GLASER P., GOFFEAN A., GOLIGHTIY E.J., GRANDI G., GUISEPPI G.,
RA HOLSAPPEL S., HOSONO S., HAIECH W.F., ITAYA M., JONES L., JONES L.,
RA ARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYSHI Y.,
RA LARDINOIS S., LAUBER J., LAZARENIC V., LEE S.M., LEVINE A., LULP H.,
RA MOSSTU D., NAKALI S., NOBAGCK M., NOONE D., O'REILLY M., OGAWA K.,
RA GUINGAS B., PRESCOTT A.M., PRESECAN E., PUTIC P., PURNELLE B.,
RA RACHOLIK S., PRESCOTT A.M., PRESECAN E., PUTIC P., PURNELLE B.,
RACHOLIK S., REY M., SADAIE Y., SERIGUCHI J., SEKONSKA A., SEROR S.J.,
RA TAKAHASHI H., TAKEMARU K., TAKENCHI M., TAMANGE R., SCOFFONE F., SERIGUCHI J., SEKONSKA A., SEROR S.J.,
RA TERPETRA P., TOGNONI A., TOSATO V., UCHITAMA S., VANDENBOL M.,
VANNIER F., VASSAROTI A., VIRRI A., VANBENDE R., VANDENBOL R.,
VANNIER F., VASSAROTI A., VIRRI A., VANBENDE R.,
RA SAGIMOTO K., YATA K., YOSHIRAM A., YONSTEIN E.,
RA VOSHIKAMA H., DANCHIRA A., YONSTEIN R.,
RA VOSHIKAMA H., DANCHIRA A.,
RA VARIN R.,
RA VIRRI R., YOSHIDA K., YOSHIRAWA H.F., ZUMSTEIN E.,
RA VOSHIKAWA H., DANCHIRA A.,
RA VARIN R., VOSHIRA A., YOSHIRA A., YONDENBOL R.,
RA VOSHIKAWA H., PANCHIRA A., VIRRI A., VANDENBOL R.,
RA VOSHIKAWA H., PANCHIRA A., VIRRI A., VANDENBOL R.,
RA VOSHIKAWA H., PANCHIRA A., VOSHIKAWA H.F., ZUMSTEIN E.,
RA VOSHIKAWA H., PANCHIRA A., VIRRI A., VANDENBOL R.,
RA VOSHIKAWA H., PANCHIRA A., VIRRI A., VANDENE R.,
RA VOSHIKAWA H., PANCHIRA A., VIRRI A., VANDEN R.,
RA VOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                          BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 294043; E313126; -.
EMBL; 299121; E1186136; -
EMPL; PF00440; tetr; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 194 AA; 22227 MW; D3457AEC CRC32;
                                                                                                                                                                       194 AA.
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98044033
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65 THFCPLE 71
                                         69 ----PLE 71
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                                                                                                                                                                                                                                                                                                                                                                     BACILLUS.
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                                                                                                                                                         00700
                                                                                                             RESULT 15
007001
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Gaps

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Query Match

8.2%; Score 89; DB 9; Length 194;
Best Local Similarity 31.0%; Pred. No. 0.8;
Matches 18; Conservative 17; Mismatches 21; Indels

Search completed: June 9, 1999, 13:00:33 Job time: 9152 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

June 9, 1999, 12:59:17; Search time 23.43 Seconds (without alignments) 178.687 Million cell updates/sec Run on:

US-08-486-814-19

Perfect score: Title:

1 MSRLDKSKVINSALELLNEV.....FGLELIICGLEKQLKCESGS 207 Scoring table: :eduence:

162890 seqs, 20225328 residues Searched:

A_Geneseq_34:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	tated In-10 de	ed Tn-10 der	ed rever	d Tet repi	Protein encoded by	Protein encoded by	O'	ד	Wild-type E.coli T	Multi-chimeric tra	meric	Protein encoded by	Sednence of the te	tTAs transactivato	tTAs transactivato	Plasmid pASK75 ope	Tetracycline trans	Pleckstrin homolog	rans	pTet-tTAk encoded	ed Tet	tetr	ed Tet	Tet	Tet	Tet	ed Te	Tet	Tet		Tet	ed Tet r	ted Tet r	ted Tet repre	Tet repre	Tet repre	Tet repre	Tet r	Tet r	ed Tet r	ted Tet repres	н	repre
SUMMARIES		R89	88	WOB	30M	W7	W7	R64	R89	W W	W48	W4	M	R4	R64	88	R8	WZ	WS	R8	Ď.	WO	K	<u>M</u>	8	×	8	8	MQ M	8	8	8	M M	8	8	8	8	W	8	8	W	3	3	M
	ē	335	207 1																																									
ı	* Query Match	100	ı ,–ı	100	100	100	100	86	86	86	86	86	86	97	97	97	6	6	6	6	6	6	5	5	5	ŏ	ŏ	ŏ	ŏ	ō	ō	ō	ō	6	9	σ	0	6	6	σ	0	0	σ	0
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	sul a		12	e	*	S	9	7	00	6	10	11	12	13	14	15	16	17	- 12	6	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	3.6	4 0	41		43

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Gaps

; 0

100.0%; Score 1080; DB 1; Length 335; 100.0%; Pred. No. 6.8e-115; ative 0; Mismatches 0; Indels 0

Query Match
Best Local Similarity 100.0
Matches 207; Conservative

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ò q R89764 standard; Protein; 207 AA. R89764;

RESULT R89764 ID R89 AC R89

61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120

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1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60

C pleitropic effects or cytotoxicity in eukaryotic cells. This
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Mutated reverse Tet repressor/VP16 fusion protein.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model.
 07-JUL-1996 (first entry)
Mutated Tn-10 derived Tet repressor.
Tet repressor: Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
                                                                                                                                                                                                                                                                                             Claim 44: Page 80: 112pp; English.

Fusion proteins comprising a first polypeptide which binds to a tet operator sequence in the presence of tetracycline or a tetracycline analogue, operatively linked to a second polypeptide which either to activate or inhibit transcription in eukaryotic cells may be used to activate or inhibit transcription. Such proteins may be used to gene therapy and for expression of gene products in transgenic organisms. Induction of gene expression is rapid, efficient and strong, typically 1000-2000 fold. The inducing agent does not cause strong, typically 1000-2000 fold. The inducing agent does not cause sequence is a mutated In-10 tet repressor used in a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DRHHTHECPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tetracycline-regulated transcription modulators - comprising
fusion proteins which bind to tet operator sequences to activate or
inhibit transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 207;
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/note= "Lys replaces wild-type Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1080; DB 1; 100.0%; Pred. No. 3.4e-115;
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/note= "reverse tet repressor" 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibiting fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207; Conservative
                                                                                                                                                        03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
                                                                                                                29-JUN-1995; U08179.
01-JUL-1994; US-270637.
15-JUL-1994; US-275876.
                                                                                                                                                                                                                 Bujard H, Gossen M;
WPI; 96-087666/09.
N-PSDB; T11352.
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                                                                         Transposon Tn-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AA;
                                                                                                                                                                                    (BUJA/) BUJARD H.
                                                                                                                                                                                                  (GOSS/) GOSSEN M
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                                                          transcription.
                                                                                  WO9601313-A1.
                                                                                                  18-JAN-1996
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Wucleic acid encoding tetracycline-inducible transcription

PT Wucleic acid encoding tetracycline-inducible transcription

regulatory fusion protein - comprising modified tetracycline

regulatory fusion protein - comprising modified tetracycline

PT Fergulator, useful for modulating eukaryotic gene expression

Rample 1: Page 77-78; 117pp; English.

WAR293 represents a Treverse" Tet repressor (TTEtR), i.e. a wild-type

controlled of vp16 (herpes simplex virus virion protein 16), a

transcriptional activator. The fusion protein forms a Tc-controlled

cranscriptional activator (TTA). The main invention of the

cranscriptional activator (TTA). The main invention of the controlled

cranscriptional activator (TTA). The main invention of the control

cranscriptional activator (TTA). The main invention of the procein

cranscription concerns modified TetR proteins that the controlled produced into a cell and used to control transcription of the protein can be

controlled by altering the concu. of tetracycline (or an analogue) in

cranscription concerns is also useful for the produce or expression in

cranter the study of disease and also for transgenic animal

criducible system is also useful for the produce or the study of gene

crantering differentiation. The Tc-inducible system allows

controlled concus. of inducer are not required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                              "C-terminal fragment of VP16 protein"
                                                                                                                                                                                                                                                                                                                                     rd H, Gossen M, Helbl V, Hillen W, Schnappinger D; 97-052305/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                /note= "Asp replaces wild-type Gly" 208. .335
                                           'note= "Asn replaces wild-type Asp"
                                                                                                         'note= "Ser replaces wild-type Leu"
                                                                                     /label- substitution
                          /label= substitution
                                                                                                                                                 /label= substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207; Conservative
                                                                                                                                                                                                                                                                                             US-485971.
                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                          06-JUN-1996; U09049
                                                               misc_difference 101
                                                                                                                           misc_difference 102
  misc_difference 95
                                                                                                                                                                                                                                                                                       07-JUN-1995; US-
(BADI ) BASF AG.
                                                                                                                                                                                                                           WO9640892-A1.
                                                                                                                                                                                                                                                                                                                                     Bujard H,
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Best Local 9
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W71323

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W08297 represents a mutated Tet repressor (TetR). This sequence was used to create a fusion protein, comprising the mutated TetR fused to a verbA silencer domain (see 145728). The fusion protein forms a Ter-controlled transcriptional activator (TTA). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator sequences tetO-4c and tetO-6c (see T45711 and re4018). Modified TetR proteins can be fused to any transcription or regulatory polypeptide and used to control transcription of a tetO-4c or tetO-6c linked gene. Nucleic acid encoding such a fusion protein or tetO-6c linked gene. Nucleic acid encoding such a fusion protein or be introduced into a cell and transcription of the protein can be controlled by altering the concor. Of tetracycline (or an analogue) in the cell, as appropriate. This ability to modulate gene expression in a protein prode in cultured cells or transgenic animals. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tc-inducible system is also useful for the prodn. of transgenic animal models for the study of disease and also for the study of gene function e.g. during differentiation. The Tc-inducible system allows rapid activation of gene transcription without cellular toxicity, high concns. of inducer are not required.
Mutated Tet repressor.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible;
repressor; gene expression; therapy; transgenic animal; disease model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-052305/05.

WPI; 97-052305/05.

Nucleic acid encoding tetracycline-inducible transcription regulatory fusion protein - comprising modified tetracycline repressor able to bind mutant tet operator, fused to transcription regulator, useful for modulating enkaryotic gene expression Example 5; Page 86-87; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossen M, Helbl V, Hillen W, Schnappinger D;
                                                                                                                                                                                                                                                                                                                                    /label= substitution
/note= "Asp replaces wild-type Gly"
                                                                                                                                                                                                                                                                                          /note= "Ser replaces wild-type Leu"
                                                                                                                                                     'note= "Lys replaces wild-type Glu'
                                                                                                                                                                                                                      'note= "Asn replaces wild-type Asp'
                                                                                                                                                                                                      /label= substitution
                                                                                                                                                                                                                                                                     /label= substitution
                                                                                                                                  /label= substitution
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995; US-485971.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996.
06-JUN-1996; U09049.
                                                                                                                                                                                                                                              misc_difference 101
                                                                                                                                                                            misc_difference 95
                                                                                                             misc_difference 7
                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                WO9640892-A1
                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bujard H,
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                                                                                                                                                               61 DRHTTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                  121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                             DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                       Gaps
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100.0%; Score 1080; DB 1; Length 207; 100.0%; Pred. No. 3.4e-115; tive 0; Mismatches 0; Indels 0;
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                                        Matches 207; Conservative
       Query Match
Best Local Similarity
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RESULT

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Example 1; Columns 67-68; 63pp; English.

Example 1; Columns 67-68; 63pp; English.

The present sequence is encoded by a "reverse" Tet repressor (rTetR), which binds to its target DNA in the presence rather than the absence of tetracycline. The sequence was generated by chemical mutagenesis.

TetR is used in the course of the invention. The specification of escribes a method for regulating expression of a Tet (tetracycline) operator-linked gene in a cell of a subject. The method comprises introducing into the cell a nucleic acid encoding a fusion protein comprising a polypeptide which binds to a Tet operator sequence, comprising a polypeptide which binds to a Tet operator sequence, transcription in eukaryctic cells, the fusion protein comprising a polypeptide which binds to a Tet operator sequence, transcription in eukaryctic cells and modulating the concentration of a tetracycline (analogue) in the subject. The method is used for the regulation of gene expression system, using tetracycline (analogues).

The system enables a gene coupled to the system to be induced in the presence of Tet and then stopped when Tet is removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1080; DB 1; Length 335; 100.0%; Pred. No. 6.8e-115; tive 0; Mismatches 0; Indels 0;
                               04-DEC-1998 (first entry)
Protein encoded by "reverse" Tet repressor sequence.
Ett repressor; rTetR; tetracycline; regulation; expression;
Tet operator-linked gene.
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W71327;
W71323 standard; Protein; 335 AA
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                                                                                                                                                                                                                                      US-260452.
US-270637.
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06-FEB-1995; US-383754.
(BADI ) BASF AG.
(KNOL ) KNOLL AG.
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                                                                                                                                                                                  US-485978
                                                                                                                                                                                                     US-076327
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Bujard H, Gossen M;
WPI; 98-541795/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the antibiotic
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; V6007
                                                                                                            Synthetic.
US5814618-A.
29-SEP-1998.
                                                                                                                                                                 07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                            01-JUL-1994;
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The present sequence is encoded by a mutant Tn10-derived tet repressor.

It is used in the course of the invention. The specification describes a method for regulating expression of a Tet (tetracycline) operator-linked gene in a cell of a subject. The method comprises introducing into the gene in a cell of a subject. The method comprises introducing into the transcription in eukaryotic cells, the fusion protein comprising a polypeptide which binds to a Tet operator sequence, operatively linked to heterologous second polypeptide which inhibits transcription in the subject. The method is used for the regulation of a tetracycline (analogue) in the subject. The method is used for the regulation of gene expression system, using tetracycline (analogues). The system canal then stopped when Tet is removed.

Tet and then stopped when Tet is removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tTA; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; qene regulation; gene therapy; tetracycline-resistance; tetR; transgenic animal.
                                                                                                                                                                                                                                                                                                                                           Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1080; DB 1; Length 207; 100.0%; Pred. No. 3.4e-115; Live 0; Mismatches 0; Indels 0;
 repressor; tetracycline; regulation; expression; operator-linked gene; tet operator.
                                                                                                                                                                                                                                                                                                                                                                                               the antibiotic
Claim 9; Columns 81-82; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus K12, KOS.
WO9429442-A.
22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1995 (first entry)
tTA transactivator.
                                                                                       07-JUN-1995; 485978.

07-JUN-1995; US-485978.

14-JUN-1993; US-076327.

14-JUN-1993; US-076726.

14-JUN-1994; US-270657.

15-JUL-1994; US-270637.

15-JUL-1994; US-270637.

15-JUL-1994; US-270637.

16-FEB-1995; US-383754.

(RNDL.) KNOLL AG.
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                                                                                                                                                                                                                                                                                          Gossen M;
                                                                                                                                                                                                                                                                                                        98-541795/46.
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                                                                                                                                                                                                                                                                                                                          N-PSDB; V60089
                                                                         29-SEP-1998
                                                                                                                                                                                                                                                                                      Bujard H,
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R64808
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(LTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal Disclosure; Page 46.48: 103pp; English.
A 397 bp Mlul/Fok! Iragment of pmSvP16 coding for the C-terminal 130 amino acids of VP16 of HSV was blunted and inserted in pUHD14-1. The resulting plasmid, pUHD15-1, encoded a terk-VP16 fusion protein, or tetracycline-controllable transactivator (tTA), whose sequence is given in Q76264, and the encoded protein sequence in R64808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CQQGFSLENALYALSAVGHFTLGCVLEDQERQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  New tetracycline-regulated transcription modulators - comprising fusion proteins which bind to tet operator sequences to activate or inhibit transcription (laim 38; Page 78; 112pp; English.
Fusion proteins comprising a first polypeptide which binds to a tet operator sequence in the presence of tetracycline or a tetracycline analogue, operatively linked to a second polypeptide which either analogue, operatively linked to a second polypeptide which either cativates or inhibits transcription in eukaryotic cells may be used to activate or inhibit transcription. Such proteins may be used to regulate gene expression in cells and may be particularly useful for gene therapy and for expression of gene products in transcent organisms. Induction of gene expression is rapid, efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1996 (first entry)
Wild type Tn-10 derived Tet repressor.
Tet repressor; Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
                                                                                                               Regulatory systems using tetracycline-controllable transactivator
                                                                                                                                                                                                                                                                                                                                          Length 335;
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                    98.0%; Score 1058; DB 1;
98.1%; Pred. No. 2.2e-112;
tive 2; Mismatches 2;
                                                        Gossen M, Salfeld JG, Voss JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity 98.1 tes 203; Conservative
14-JUN-1994; U06734.
14-JUN-1993; US-076327.
(BADI ) BASF AG.
Bujard H, Gossen M, Sz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1994; US-275876
03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1995; U08179.
01-JUL-1994; US-270637.
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                                                                                                                                                                                                                                                                                 335 AA:
                                                                        WPI; 95-036472/05.
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N-PSDB; T11351.
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W09601313-A1.
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                                                                                           N-PSDB; Q76264.
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                                                                                                                                                                                                                                                                                 Sequence
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regulatory fusion protein - compension modified tetracycline regulatory fusion protein - compension modified tetracycline regulatory fusion protein - compension modified tetracycline regulator, useful for modulating eukaryotic gene expression regulator, useful for modulating eukaryotic gene expression regulator, useful for modulating eukaryotic gene expression for modulating eukaryotic gene expression (Transposon IO (Thil)) of E. coli. The wild-type sequence is used for the production of a mutated TetR (so as to bind its target in the presence rather than the absence of tetracycline). Mutant TetR proteins can be fused to a transcriptional activator e.g. VP16 (herpes simplex virus virion protein 16), to form a Tc-controlled transcriptional activator (TRA). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator activator (TRA). The main invention of the specification concerns modified retR proteins that bind to modified class B tet operator sequences tetCo-4C and tetCo-6C (see T45711 and T48478). Modified TetR proteins can be fused to any transcription regulatory polypeptide and used to control transcription of a tetO-4C or tetO-6C linked gene.

Nucleic acid encoding such a fusion protein may be introduced into a cell and transcription of the protein can be controlled by altering the control transgenic animal models for the study of disease and also for the study of gene function e.g. during differentiation. The Tc-inducible system allows rapid activation of gene transcription e.g. during differentiation.

To inducible system allows rapid activation of gene transcription controlled.
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Tet; tetracycline; Tc; operator; transcription; regulation; inducible;
repressor; gene expression; therapy; transgenic animal; disease model;
                                                                                                                                                                                                                                                                                                                                                               61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPFLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                      61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                          1 MSRLDKSKVINSALELLNEVGIEGLFTRKLAQKLGVEQPFLYWHVKNKRALLDALAIEML 60
strong, typically 1000-2000 fold. The inducing agent does not cause pleitropic effects or cytotoxicity in eukaryotic cells. This sequence is the wild type Tn-10 tet repressor.
                                                                                                                                                                                              ö
                                                                                                                                            Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bujard H, Gossen M, Helbl V, Hillen W, Schnappinger D; WPI; 97-052305/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding tetracycline-inducible transcription
                                                                                                                                                                                              Indels
                                                                                                                                                                                              5;
                                                                                                                                            Score 1058; DB 1;
Pred. No. 1.1e-112;
                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                          98.0%;
98.1%;
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                                                                                                                                                                                           Matches 203; Conservative
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06-JUN-1996, U09049.
07-JUN-1995; US-485971.
(BADI ) BASF AG.
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                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
WO9640892-Al.
                                                                                                                                               Query Match
                                                                          Sequence
                                                                                                                                                                        Best Local
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and envelope protein

Sicologues: Fig 4A-C: 84pp; English.

This fusion protein comprises a multi-chimeric transactivator, designated rTAER, that is composed of (from the N-terminus to the casignated rTAER, that is composed of (from the N-terminus to the transcriptional activation domain of herpes simplex virus VD16, and the ligand binding domain of the oestrogen receptor. An inducible expression system of the invention is composed of tTAER and a minmal promoter (see V1775) derived from the immediate early gene of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be converted to a nuclectide sequence of interest. The invention relates to packaging cell lines derived from HeLa. DI7, MDCK, BHK or preferably Cf2Th cells and recombinant retroviral particles.

Produced by them, particularly pseudotyped retroviral particles.

Produced by them, particularly pseudotyped retroviral particles.

Produced by them inducible expression system. The products can be used for the inducible expression in cells of polypeptides, e.g. cytotoxic products or therapeutic agents. The activation of the inducible expression system requires 2 independent signals, thus contains the inducible expression for the inducible expression for the inducible expression system requires 2 independent signals, thus contains the inducible expression for the inducible expression for the inducible expression for election of the inducible expression system requires 2 independent signals, thus contains the inducible expression for the inducible expression for the inducible expression system requires 2 independent signals, thus contains the inducible expression for the inducible expression for the inducible expression for the inducible e
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                                                                                                                                                                                                                           61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                          Gaps
                                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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comprises sequences encoding retroviral Gag and Pol polypeptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multi-chimeric transactivating factor rTAER fusion protein. Multi-chimeric transactivating factor; rTAER; tetR; tetR; tetracycline repressor; HSV; oestrogen receptor; promoter; packaging cell line; retrovirus; retroviral particle; vector;
Length 207;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1998.
06-AUG-1997; UJ3846.
07-AUG-1996; US-694652.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
Chen S, Friedmann T, Miyanohara A, Prussak CE, Yee J; N-PSDB; V17756.
Score 1058; DB 1;
Pred. No. 1.1e-112;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Herpes simplex virus.
Chimeric - Mammalia.
WO9805759-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W48357 standard; Protein; 651 AA
98.0%;
98.1%;
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Chimeric - Escherichia coli.
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Query Match
Best Local Similarity 98.1
Matches 203; Conservative
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Sequence 65
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Gaps

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98.0%; Score 1058; DB 1; Length 651; 98.1%; Pred. No. 5.6e-112; ive 2; Mismatches 2; Indels (

Query Match 98.0° Best Local Similarity 98.1° Matches 203; Conservative

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PT New inducible expression systems - comprising multi-chimeric transactivator, induces transcription from promoter in the absence of first ligand and presence of second ligand moder in the absence of first ligand and presence of second ligand

Example 1: Fig 4: 72pp: English.

Example 1: Fig 4: 72pp: English.

The sequence is that of multi-chimeric transcription activational domain of the E.coli tetR polypeptide, the transcription activational domain of HSV VPI6 and the ligand-binding domain of an oestrogen receptor from pHEI4 (Kumar et al. 1986). DNA encoding it can be used as part of an inducible expression system which induces transcription from the promoter in the absence of the first ligand and presence of the common of the products can be used for the inducible expression in cells of polypeptides such as cytotoxic products or therapeutic products.

The activation of the inducible expression system requires 2 independent signals, which reduces the incidence of undesired transcriptional activation.
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                                                                                          61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                     DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL
MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
                                                                                                                                                                                                                                                                                                                                                                                     Multi-chimeric transactivator trAER sequence. inducible expression system; modulation; cytotoxin; therapeutic; trAER; multi-chimeric; transactivator; tetR; Vp16; ligand-binding domain.
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Pred. No. 5.6e-112;
2; Mismatches 2; Indels (
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W47583;
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1996; US-693940.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus. WO9805754-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1998.
29-JUL-1997; U13221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
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claim 4: Columns 77-80; 63pp; English.

The present sequence is encoded by wild type Inl0-derived tet repressor. It is used in the course of the invention. The specification describes a method for regulating expression of a Tet (tetracycline) operator-linked gene in a cell of a subject. The method comprises introducing into the cell a nucleic acid encoding a fusion protein which inhibits transcription in eukaryotic cells, the fusion protein comprising a polypeptide which hinds to a Tet operator sequence, operatively linked to heterologous second polypeptide which inhibits transcription in eukaryotic cells and modulating the concentration of a tetracycline (analogue) in the subject. The method is used for the regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression system, using tetracycline (analogues). The system enables a gene coupled to the system to be induced in the presence of Tet and then stopped when Tet is removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                         04-DEC-1998 (first entry)
Protein encoded by wild type Tn10-derived tet repressor.
                                                                                                                                                                                                                         Tet repressor; tetracycline; regulation; expression;
Tet operator-linked gene; tet operator.
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                                                                        W71326 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                  Unidentified.
USS814618-A.
29-SEP-1998.
07-UNN-1995; US-485978.
14-UNN-1995; US-076327.
14-UNN-1994; US-07626.
14-UNN-1994; US-260452.
15-UL-1994; US-275876.
06-FEB-1995; US-383754.
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1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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Matches 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tTAS transactivator.

tTA: tTAS; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; teransgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                         the NheI
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                                                                                                                                                                              Tetracycline repressor-mediated regulation system - useful for controlling gene expression in transgenic animals Disclosure; page 41-42; 76pp. English.

The inventors claim a construct which comprises an animal promoter element having a tetracycline repressor (tetR) operator. The promoter alement may be the PEPCK promoter which is tissue specific promoter alement may be the PEPCK promoter which is tissue specific shortly prior to birth. The tetR sequence in the construct is 3' to a TATA-box sequence and is inserted into the NheI site of the PEPCK promoter element. The entire sequence of the tetR sequence 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transactivator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulatory systems using tetracycline-controllable transactive (tTA) - useful for conditional inactivation or modulation of yene expression in a host cell or animal bisclosure; Page 50-51; 103pp; English.
A DNA fragment of pMSVP16 coding for the C-terminal 97 amino
                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.5%; Score 1053; DB 1; Length 207; Best Local Similarity 97.6%; Pred. No. 4e-112; Matches 202; Conservative 2; Mismatches 3; Indels
                           Sequence of the tetracycline repressor tetR.
Tetracycline repressor; TetR; Tnl0; transposon 10.
Escherichia coli.
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WPI; 95-036472/05.
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standard; Protein; 207 AA.
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                          (first entry)
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14-JUN-1993; US-076327.
(BADI ) BASF AG.
                                                                                             03-man 1271.
26-AUG-1993; U08230.
26-AUG-1992; US-935763.
                                                                                                                                                      94-083191/10.
                                                                                                                              (DNXD-) DNX CORP.
                                                                                                                                                                     N-PSDB; Q56710.
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                          19-AUG-1994
                                                                            WO9404672-A.
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promoter linked to control excession of gene regulated by minimal promoter linked to tet operon, and vectors and cells where gene expression is regulated by tetracycline expression is regulated by tetracycline bisclosure; Fig 5A-B; 37pp; English.

A fusion protein (R85324) composed of the Escherichia coll Th10 tet repressor (tetR) and a 127-amino acid C-terminal portion of the transactivation activating domain of herpes simplex virus virion protein 16 (VP16) is the product of novel tetracycline-controlled transactivator tTA (T06868). The transactivator is used to regulate expression of a heterologous gene operably linked to a minimal promoter cerived from human cytomegalovirus promoter IE (see T06869-70) and at least i tet operator (tetC) sequence. On/off regulation of expression of a the heterologous protein by host eukaryotic cells is provided by carlying the medium tetracycline conc. Transgenic animals producing a desired protein in their milk can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
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acids of VP16 of HSV was blunted and inserted in pUHD14-1. The resulting plasmid, pUHD151-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (smaller version, tTAS), whose sequence is given in Q76265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transactivator; tTAs; tet repressor; tetR; virion protein 16; VP16; gene expression; tetracycline-responsive promoter;
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                                                                                                                                                                                                                                                        Length 297;
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Pred. No. 6.7e-112;
2; Mismatches 3;
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Chimeric Herpes simplex virus.
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Best Local Similarity 97.6%;
Matches 202; Conservative
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14-JUN-1993; 076726.
14-JUN-1993; US-076726.
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95-392612/50.
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- 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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Search completed: June 9, 1999, 12:59:17 Job time: 9196 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 9, 1999, 12:59:50 ; Search time 19.42 Seconds (without alignments) 399.294 Million cell updates/sec

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEVFGLELIICGLEKQLKCESGS 207 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 116738 seqs, 37460341 residues Searched:

PIR_58:* Database:

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pirl:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180

DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120

ò g οχ g δλ q δ g regulatory protein tetR - Escherichia coli plasmid RA1
N;Alternate names: tet repressor class D
C;Species: Escherichia coli
C;Date: 07-Sep-1990 *text_change 12-Jun-1998
C;Accession: S07359
R;Unger, B.; Klock, G.; Hillen, W.
Nucleic Acids Res. 12, 7693-7703, 1984
A;Title: Nucleotide sequence of the repressor gene of the RA1 tetracycline resistance

hypothetical prote probable transcrip hypothetical prote hypothetical prote transcription regu hypothetical prote
S12393 E70873 S50608 F64100 F69985
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188 187 1391 187 194
7.7.7.7. 4.4.6.6.6.
80 80 79.5 79 79
44444 12444 14444 1444

ALIGNMENTS	RESULT 1 RPECTN repressor tetR - Escherichia coli transposon Tn10 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Berberichia coli C;Species: Nau-1987 #sequence_revision 17-Mar-1987 #text_change 12-Jun-1998 C;Accession: A03576; S02667 R;Postle, K.; Nguyen, T.T.; Bertrand, K.P. Nucleofic Acids Res. 12, 4849-4863, 1984 A;Title: Nucleotide sequence of the repressor gene of the TN10 tetracycline resistanc A;Reference number: A03576; MUID:84247342 A;Accession: A03576 A;Molecule type: DNA A;Residues: 1-207 <pos> A;Accession: No. BABO J. 7, 4011-4017, 1988 A;Title: A threonine to alanine exchange at position 40 of tet repressor alters the r A;Recence number: S02667; MUID:89091153 A;Accession: S02667;</pos>	A Status: not compared with conceptual translation A Molecule type: DNA A Molecule type: DNA A Residues: 1-100 CALT> A Cross-references: GB:J01830; NID:g154845 C;Comment: This protein contains sequences similar to the DNA recognition regions of C;Genetics: A Genetics: A Gene: tetR C;Superfamily: tetracycline repressor C;Keywords: antibiotic resistance: DNA binding; transcription regulation F;25-46/Region: helix-turn-helix #status predicted	Query Match 97.5%; Score 1053; DB 1; Length 207; Best Local Similarity 97.6%; Pred. No. 2.2e-91; Matches 202; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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                                                                                                                                                                                                                                                                                                           61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                               C;Superfamily: tetracycline repressor
C;Keywords: antibiotic resistance; DNA binding; transcription regulation
F;25-46/Region: helix-turn-helix #status predicted
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C:Cross-references: EMBL:X65876; NID:g49073; PID:g49075
C:Genetics:
A:Genetics:
A:Gene: tetR
A:Gene: plasmid
C:Superfamily: tetracycline repressor
C:Keywords: antibiotic resistance; DNA binding; transcription regulation
F:25-46/Region: helix-turn-helix #status predicted
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                                                                                                                                                                                                                               Length 218;
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                                                                                                                                                                                                                                                      Matches 128; Conservative 27; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory protein tetR - Salmonella ordonez plasmid pIP173
N.Alternate names: tetracycline repressor
                                                              A, Cross-references: EMBL:X01083; NID:943053; PID:943054
                                                                                                                                                                                                                         61.6%; Score 665; DB 2;
63.7%; Pred. No. 4.4e-55;
A; Reference number: S07359; MUID: 85037938
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                                   A: Molecule type: DNA
A; Residues: 1-218 <UNG>
                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                    A; Genome: plasmid
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                   A; Accession:
                                                                                                     A;Gene: tetR
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Best Local 3
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tetracycline resistance protein - Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Accession: A26948 #sequence_revision 19-Nov-1988 #text_change 12-Jun-1998
R;Heuer, C.; Hickman, R.K.; Curiale, M.S.; Hillen, W.; Levy, S.B.
J. Bacteriol. 169, 990-994, 1987
A;Title: Constitutive expression of tetracycline resistance mediated by a Tn10-like A;Reference number: A26948; MUID:87137315
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Mol. Biol. Evol. 2, 1-12, 1985
A. Filer The tracycline repressor of pSC101.
A. Accession: A03575
A. Filer Every Mulb. 88216101
A. Accession: A03575
A. Filer Coule type: DNA
A. Residues: 1-219 - CBRO>
A. Cross-references: GB:M36272; NID:g150945; PID:g150946
C. Comment: This protein is the repressor of the tetracycline resistance element; its
A. Genetics:
A. Genetics:
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C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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C.Superfamily: tetracycline repressor
C.Superfamily: tetracycline resistance; DNA binding; transcription regulation
F:24-46/Domain: DNA binding #status predicted <DBN>
F:25-46/Region: helix-turn-helix #status predicted
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47.4%; Score 512; DB 1; Length 219;
Best Local Similarity 51.7%; Pred. No. 8.9e-41;
Matches 105; Conservative 33; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 597; DB 2; Length 120 92.0%; Pred. No. 4.9e-49; 1ive 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: M15539; NID: 9148988; PID: 9148989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Superfamily: tetracycline repressor
F:25-46/Region: helix-turn-helix #status predicted
                                              181 DGEQAFLHGLESLIRGFEVQL 201
181 GAEPAFLFGLELIICGLEKOL
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Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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A; Residues: 1-216 <TRU>
A; Residues: 1-216 <TRU>
A; Cross-references: EMBL:X75761; NID:g415984; PID:g415985
C; Superfamily: tetracycline repressor
F; 25-46/Region: helix-turn-helix #status predicted
A; Reference number: S38655
                  A; Accession: S38655
A; Status: preliminary
A; Molecule type: DNA
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A;Reference number: JQ1475; MUID:92192465
A;Accession: JQ1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Cross-references: EMBL:X61367; NID:g48194; PID:g48198
A.Kross-references: EMBL:X61367; NID:g48194; PID:g48198
A.Note: the authors translated the codon GAG for residue 19 as Asp and CAG for residue 8 R:Altschmided, L.; Baumeister, R.; Pfleiderer, K.; Hillen, W.
EMBO J. 7, 4011-4017, 1988
A.Title: A threonine to alanine exchange at position 40 of tet repressor alters the recc A:Reference number: S02667; MUID:89091153
A:Reference number: S02668
A:Status: not compared with conceptual translation
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Jun-1998
C;Accession: S38655
R;Trueman, P; Sharpe, G.S.; Barth, P.T.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: tetracycline resistance repressor
C;Species: Escherichia coli
C;Detc: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 12-Jun-1998
C;Accession: JO1478; S02668; S24113
R;Allmeier, H.; Cresnar, B.; Greck, M.; Schmitt, R.
Gene 111, 11-20, 1992
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                61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL
                                                                                                     CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.8%; Score 505.5; DB 2; 51.5%; Pred. No. 3.5e-40;
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A.Residues: 1-100 <ALT>
C.Genetics:
A.Gene: tetR
C.Superfamily: tetracycline repressor
F.25-46/Region: helix-turn-helix #status predicted
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tet repressor protein (Tn 1721) - Escherichia coli plasmid RP1
C;Species: Escherichia coli
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 12-Jun-1998
C;Accession: A03574
R;Waters, S.H.; Rogowsky, P.; Grinsted, J.; Altenbuchner, J.; Schmitt, R.
Nucleic Acids Res. 11, 6089-6105, 1983
A;Titler The tetracycline resistance determinants of RP1 and Tn1721: nucleotide seque
A;Reference number: A93486; MUID:83299270
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C;Keywords: antibiotic resistance; DNA binding; transcription regulation
F;25-46/Region: helix-turn-helix #status predicted
                                                                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
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  Length 216;
     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-216 <MAT>
A;Cross-references: GB:X00006; NID:g42508; PID:g42509
                            .5e-40;
        DB
46.8%; Score 505.5;
51.5%; Pred. No. 3.5e
tive 35; Mismatches
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180 EAGPDAAFEQGLAVIVDGLAKR 201
                            Best Local Similarity 51.5%
Matches 104; Conservative
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Matches 102; Conserv
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probable transcription repressor mtrR - Neisseria gonorrhoeae (strain CH95)
C;Species: Neisseria gonorrhoeae
C;Species: Neisseria gonorrhoeae
A;Variety: strain CH95
C;Date: (07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Accession: 843417; 840251
Nol. Microbiol. 11, 769-775, 1994
A;Title: Regulation of the permeability of the gonococcal cell envelope by the mtr sy A;Reference number: 842417
A;Residues: 01-210 cpan.
A;Accession: 842417
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-210 cpan.
A;Residues: 1-210 cpan.
A;Experimental source: CH95
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUD:98196666 A;Accession: C70487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-192 <AQF>
A;Residues: 1-192 <AQF>
A;Crossreferences: GB:AE000776; NID:g2984355; PID:g2984362; GB:AE000657
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription regulator TetR/AcrR family - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998
C;Accession: C70487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CIAQDAADAEGGSWIVF-RHILLHFFERLQSNDIYYKFH-------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 EH--TEQNA--AVIAIA-------RKHQAIWREKIT------AVLTEAVENQDLAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.8%; Score 105.5; DB 2; Length 2
Best Local Similarity 26.8%; Pred. No. 0.0086;
Matches 51; Conservative 23; Mismatches 73; Indels
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Best Local Similarity
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156 DLDKETAVIF 165
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C:Species: Neisseria gonorrhoeae
A:Variety: strain FA19
C:Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
A:Pan, W.: Spratt, B.G.
A:Pan, Marcobiol. 11, 769-775, 1994
A:Pan
                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-191 <KUN>
A;Cross-references: GB:299114; GB:AL009126; NID:92634230; PID:e1185379; PID:92634300
A;Experimental source: strain 168
C;Genetics:
A;Gene: yobS
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        A;Reference number: A69580; MUID:98044033
A;Accession: A69900
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LDRHHTHFCPLKGES------WQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 FDQMADSVTERKGDSAMLSLAHAYVDFAIENPGYYEAALL-----KVH------DKRTE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 TLENQLAFLCQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
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9.9%; Score 106.5; DB 2; Length 210;
Best Local Similarity 26.8%; Pred. No. 0.0069;
Eatches 51; Conservative 23; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 11.4%; Score 123; DB 2; Length 191; I Similarity 24.1%; Pred. No. 0.00018; 49; Conservative 38; Mismatches 74; Indels
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-210 <PAN>
A:Cross-references: EMBL:Z25797; NID:g452332; PID:g438189
A:Experimental source: strain FA19
C:Genetics:
A:Gene: mirR
C:Superfamily: probable transcription repressor mtrr
C:Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 PLLRQAIELFDHQGAEPAFLFGL 190
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Best Local Similarity
Matches 49; Conserva
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Gaps

43;

Length 210;

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Indels 51; Gaps

Length 192;

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Search completed: June 9, 1999, 12:59:50 Job time: 9169 sec

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GenCore version 4.5
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- protein search, using sw model OM protein June 9, 1999, 13:01:02; Search time 16.52 Seconds (without alignments) 336.316 Million cell updates/sec Run on:

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Perfect score: Sequence: Title:

BLOSUM62 Scoring table: 74019 seqs, 26840295 residues Searched:

SwissProt_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	scription		P04483 escherichia	pasteurell	pasteurell	escherichi	P03039 escherichia	escher	P21337 escherichia	P51560 vibrio angu	Q11023 mycobacteri	P39897 neisseria g	P75952 escherichia	escheric				escherich	bacillus s						haemophil								g E				acan	escherich	sns		P08799 dictyosteli	Sa	caenorh	qallus	P11501 gallus gall
SOMMARIES	ΟI		E	TER8	-	TER4_	TER3	TER]	TER	TER7	X07		•			THT	KIN			TIK		CF17	YP2	N15	X85			1 ACRR_ECOLI	NIFL		_	NUM	PLZE	PHSF	CUI	FA8_	_	ATK	FA8_		MYS2		YLU	FRAZ	HS97
	engt.	1																					188	1391	187	770	218	215	519	212	192	2748	613	838	1324	2319	1509	557	2133	474	2116	892	1207	323	728
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			1053	665	663	099		505.5	o	473	w	106.5	92.5	91.5	86	84.5	83.5	83	82.5	82	81.5	80.5	80	79.5	79	78.5	78.5	78	78	77.5	77	77	77	76.5	75	75	75	74.5	74	74	74	74	74	73.5	73.5
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P08238 homo sapien	
HS9B_HUMAN	Y307_MYCPN
Н	-
723	1244
8.9	8.9
73.5	73
44	45

ALIGNMENTS

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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITH LD., BERTRAND K.P.;
J. MOL. BIOL. 203:949-959(1988).

J. MOL. BIOL.

I. FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS ANINO-TERMINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
(TETA) PROMOTER OPERATOR SITES.

-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H->Y: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N->H: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T->1: REDUCES AFFINITY FOR TETRACYCLINE LESS THAN 10 FOLD.
4AB4DD5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGNESIUM (OF [MG-TC]+ COMPLEX) SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1053; DB 1; Length 207;
Pred. No. 3.4e-92;
2; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON TN10).
                                                                                                                                                                                                            MEDLINE; 84005886.
BERTRAND K.P., POSTLE K., WRAY L.V. JR., REZNIKOFF W.S.;
GENE 23:149-156(1983).
207 AA
                      05, CREATED)
05, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 FOLD
                                                                                                                                                           POSTLE K., NGUYEN T.T., BERTRAND K.P.;
NUCLEIC ACIDS RES. 12:4849-4863(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 FOLD.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 AA; 23354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%;
97.6%;
                                                                                                                                                                                                SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 202; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                              ENTEROBACTERIACEAE
                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 84247342.
                                                                                                                                                                                                                                                               MUTAGENESIS.
MEDLINE; 89094871.
                                                                                    ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
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TER2_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                     PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
              121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPILRQAIELFDHQ 180
                                                                                                                                                                                                                                                     MICROBIOL. IMMUNOL. 38:31-38(1994).

- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO TERMINAL REGION FORMS A HELIX-TURN-HELIX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 COQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                            INDUCTION: BY THE [MG-TETRACYCLINE] + COMPLEX.
SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                    H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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SIMILARITY).
3C57D4AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.6%; Score 665; DB 1; Length 218; 63.7%; Pred. No. 1.2e-55; Live 27; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                         EMBL, D16172; G575938; -. PROSITE; PS01081; HTH_TETR_FAMILY; 1. TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                   181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT ,
TERR_PASMU
ID TERR_PASMU STANLALL....
AC P51561;
AT 01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                          ANTIBIOTIC RESISTANCE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AA; 24419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GAEPAFLFGLELIICGLEKOL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 DGEQAFLHGLESLIRGFEVQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 128; Conservative
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                   PASTEURELLA PISCICIDA.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94328963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                 PASTEURELLACEAE
                                                                                                                                                                                              PLASMID PSP935
                                                                                                                                                                                                                                                                                                                                                 REGULATORS
                                                                                                              TER8_PASPI
P51562;
                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
SITE
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                                                                                          RESULT 2
TER8_PASPI
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTEURELLACEAE.
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HANSEN L.M., MCMURRY L.M., LEVY S.B., HIRSH D.C.;
ANTIMICROB. AGBYTS CHEMOTHER. 37:2699-2705(1993).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINSD DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
(TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETRACYCLINE] OF TRANSCRIPTIONAL
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM--PPLLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGNESIUM (OF [MG-TC]+ COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%; Score 663; DB 1; Length 207; 63.2%; Pred. No. 1.7e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U00792; G392872; -.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGIGNATION; REPRESSOR; DNA-BINDING; ANTIBOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45 H-T-H MOTIF (POTENTI
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A51DA28B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Mismatches
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SPECIES-E.COLI; STRAIN=J53-1; PLASMID=RA1;
MEDLINE; 85037938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESCHERICHIA COLI, AND SALMONELLA ORDONEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETRACYCLINE REPRESSOR PROTEIN CLASS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 HOGAEPAFLFGLELIICGLEKQLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (REL. 10, CREATED)
01-OCT-1996 (REL. 34, LAST SEQU
01-NOV-1997 (REL. 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AA; 23156 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
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                                                                                               PASTEURELLA MULTOCIDA
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  MEDLINE; 94153051
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                                                                                                                           PLASMID PVM111.
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SEQUENCE FROM N.A.
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                            MEDLINE;
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PLASMID PSC101.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 RHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX. SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                  HINRICHS W., KISKER C., DUEVEL C., MUELLER A., TOVAR K., HILLEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                               ALLARD J.D., GIBSON M.L., VU L.H., NGUYEN T.T., BERTRAND K.P.;
MOL. GEN. GENET. 237:301-305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H-T-H MOTIE (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+.
MAGNESIUM (OF [MG-TC]+ COMPLEX).
830EPSEE CRC32;
                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.1%; Score 660; DB 1; Length 217; 63.5%; Pred. No. 3.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; ZTRT; 20-JUN-96.
PROSCITE; PS01081; HTH_TETR_PAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTIBIOTIC RESISTANCE; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Indels
                                                           SEQUENCE FROM N.A.
SPECIES=S.ORDONEZ; STRAIN-BM2000; PLASMID=PIP173;
MEDLINE; 93204906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Mismatches
   NUCLEIC ACIDS RES. 12:7693-7703(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AA; 24287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GEQAFLHGLESLIRGFEVOL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 AEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X01083; G43054; -. EMBL; X65876; G49075; -. PIR; S07359; S07359. PIR; S30287; S30287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 2TCT; 03-APR-96.
PDB; 2TRT; 20-JUN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                         MEDLINE; 94204640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TER3_ECOLI P03030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TER3_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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         RREAR RATH RREAR R
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PLASMID RP1, AND PLASMID RP4.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BROW M.A.D., PESIN R., SUTCLIFFE J.G.;
MOL. BIOL. EVOL. 2.1-12(1985).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS ANINO-TEMBINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                   (TETA) PROMOTER OPERATOR SITES.
SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARIY).
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 219;
                                                                                                                                                                                                                             EMBL; M36272; G150946; -.
PIR; A03575; REPECYS.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID; ANTIBIOTIC RESISTANCE.
DNA_BIND 26 45 H-T-H MOTIF (POTENTIAL).
SITE 64 1NVOLVED IN RINDING PAGE 1977-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1996 (REL. 01, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS A (TRANSPOSON 1721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.4%; Score 512; DB 1;
51.7%; Pred. No. 3e-41;
tive 33; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6C9E1828 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLMEIER H., CRESNAR B., GRECK M., SCHMITT GENE 111:11-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
PLASMID=PLASMID RP4;
TRUEMAN P., SHARPE G.S., BARTH P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VYEGGPDAAFERGLALIIGGLEK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TRANSPOSON-TN1721; PLASMID-RP1;
MEDLINE; 83299270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 AA; 24174 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
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01-OCT-1996 (REL. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSPOSON=TN1721;
MEDLINE; 92192465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
88216101.
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
WATERS S.H., ROGOWSKY P., GRINSTED J., ALTENBUCHNER J., SCHMITT R.;
NUCLEIC ACIDS RES. 11:6089-6105(1983).
-!- FUNCTION: TETR TEPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERNINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CEAGFSAGDAVNALMTISYFTVGAVLEEQAGDSDAGER-GGTVEQAPLSPLLRAAIDAFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOVAR K., ERNST A., HILLEN W.;
MOL. GENGT. 215.76-80(1988).
-!- FUNCTION: TETR REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT, ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                          (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TETA) PROMOTER OPERATOR SITES.
SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                      INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                     SIMILARITY),
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                            46.8%; Score 505.5; DB 1; Length 216; 51.5%; Pred. No. 1.2e-40;
                                                                                                                                                                                                  PIR: A03574; RPECRI.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; TRANSPOSABLE ELEMENT;
DNA-BINDING; ANTIBIOTIC RESISTANCE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Indels
                                                                                                                                                                                                                                                                                                                                 SIMILARITY).

TH -> ST (IN REF. 3).

I -> T (IN REF. 3).

DA -> ES (IN REF. 3).

4; F72BDFB1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
                                                                                                                                                                                                                                                                       H-T-H MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETRACYCLINE REPRESSOR PROTEIN CLASS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 HQGAEPAFLFGLELIICGLEKQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : || || : || |: || || 180 EAGPDAAFEQGLAVIVDGLAKR 201
                                                                                                                                                                                                                                                                                                                                                              80 I
155 DA
23320 MW;
                                                                                                                                                         EMBL; X61367; G48198; -.
EMBL; X75761; G415985; -.
EMBL; X00006; G42509; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                   100
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154
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 89201249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                           REGULATORS.
                                                                                                                                                                                                                                                  DNA-BINDING; DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TER5_ECOLI
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                METAL
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PLASMID PJA8122.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                              61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                 121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                       1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                        MICROBIOL. IMMUNOL. 36:1051-1060(1992).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELLY-TURN-HELLY STRUCTURE AND BINDS DAN. BINDING OF TETRACYCLINE TO TETR REDUCES (TETA) PROMOTER OPERATOR SITES.

-!- INDUCTION: BY THE [NG-TETRACYCLINE] + COMPLEX.

-!- SIMILARITY: BELONGS TO THE TETRACYCLINE OF TRANSCRIPTIONAL
                                                                               H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                        MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                    45.7%; Score 493.5; DB 1; Length 211; 50.2%; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                   Indels
         EMBL; M34933; G155020; ALT_SEQ.
EMBL; X14035; G43056; -.
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S52438; G262929; -.
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45
                                                                                                                                                   V -> L (IN G43056).
F538C813 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811CB332 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥
                                                                                                                                                                                                                               29; Mismatches
                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                 ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45 H-
                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SAEMAFHFGLKSLIFGFSAQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                    181 GAEPAFLFGLELIICGLEKQL 201
                                                                                                                                                              211 AA; 23585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 AA; 23595 MW;
                                                                                                                                                                                                                 Best Local Similarity 50.2%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                      100
                                                                                             64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIBRIO ANGUILLARUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MZ8122;
MEDLINE; 93125225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J., AOKI T.;
                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
 REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIBRIONACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TER7_VIBAN
P51560;
                                                                                                                                              CONFLICT
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 HTHFCPLKGESWQDFLRNKAKSFR-----CALL-----SHRNGAKVHSDTRP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 VFATPYIEAGDWRETLRNHARSMRKTFADNPVLCDLILIRAALSPKTARLGA----- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 TEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ--------E 150
                                                                                                                                                                                                                                                                                                                    121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPP--LLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CAEGFCPKRAVWALRAVSHYVVGSVLEQQASDADERVPDRPDVSEQAPSSFLHVLFHELE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 INPEDIISGAFELAQQVSIDNLSMPLLGKHLGVGVTSIYWYFRKKDDLLNAMTDRALSKY 75
                                                                                                                                                                                                                                                                               61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                          Gaps
                                                                                                                                                   1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                     MURRHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Z7555; E250355; -.
PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG,
PROSITE: PS01081; HTH_TETR_FAMILY; FALSE_NEG,
PROSITE: PS01081; HTH_TETR_FAMILY; FALSE_NEG,
PROSITE: PS01081; HTH_TETR_FAMILY; FALSE_NEG,
PS01081; FAMILY; FALSE,
PS01081; FAMILY; FAMI
                          Score 473; DB 1; Length 210;
Pred. No. 1.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                          72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 HQVAKEERETPTTDSMPPLLRQAIELFDHQGA--EPAFLFGLELII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR CY02B10.17C.
43.8%; Scor.
y 47.3%; Pred. No. 1...
've 32; Mismatches ""rcvbQp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 HQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTCY02B10.17C.
MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                          95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTRR_NEIGO
P39897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YO7H_MYCTU
ID Y07H_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    011023;
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MTRR_NEIGO
                                                                                                 Matches
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SEQUENCE FROM N.A.
STRAIN-K12 / WO1655;
BLATTHER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94254732.
PAN W., SPRAIT B.G.;
MOL. MICROBIOL. 11.769-775(1994).
-!- FUNCITON: PUTATIVE REPRESSOR OF MIRC GENE. CONTROLS THE PERMEDITIY OF THE CELL ENVELOPE TO HYDROPHOBIC COMPOUNDS SUCH AS ANTIBLOTICS AND DETERGENTS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H-T-H MOTIF (POTENTIAL).
H -> Y: IN PENICILLIN-RESISTANT ISOLATES.
; F4CABF98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 CIAQDAADAEGGSWIVF-RHILLHFFERLQSNDIHYKFH-------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 EH--TEQNA--AVIAIA------RKHQAIWREKIT------AVITEAVENQDLAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 KEHLMLAALETFYRKGIARTSLNEIAQAAGVTRGALYWHFKNKEDLFDALFORICDDIEN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN NDH-MFD INTERGENIC REGION
                                                                                                                                                                      NEISSERIA GONORRHOEAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

9.9%; Score 106.5; DB 1; Length 210;
Best Local Similarity 26.8%; Pred. No. 0.0041;
Matches 51; Conservative 23; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000211; G1787354; --
BCOGENE; EG13435; YCRQ.
PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; REPRESSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z25797; G438189; -.
PIR; S40250; S40250.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BIND MG; REPRESSOR.
DNA_BIND 105 105 H -> Y: IN PENICILLI
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
REGULATORY PROTEIN MTRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 AA; 24192 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 HQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 DLDKETAVIF 165
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                  NEISSERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-BINDING
                                                                                                                                                                                                                                                                                                                                            STRAIN-FA19;
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VARIANT
SEQUENCE
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IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
RASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORIH H., MOTOWURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMEEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
SUBMITTED (DEC-1996) TO EMBL/GENDANK/DDBJ DATA BANKS.
-- FUNCTION: REPRESSOR FOR THE UIDRABC (GUSRABC) OPERON.
                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                 63 --HHTH-FCPLKG--ESWQDFLRNKAKSF------RCALLSHRNGAKVHSDTR 104
                                                                                                                                                                            106 AKHEAQLFCEEKSVESALADYFAAIANCFTSKDTPAGCFMINNCTTLSPDSGDIANTLKS 165
                                                                                  Gaps
                                                                                                  5 DKSKVINSALELLNEVGIEGLITTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KSKVINSALELLNEVGIEGLITRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                Query Match
8.6%; Score 92.5; DB 1; Length 236;
Best Local Similarity 25.2%; Pred. No. 0.098;
Matches 35; Conservative 18; Mismatches 63; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 91.5; DB 1; Length 196; 24.0%; Pred. No. 0.097; Live 24; Mismatches 32; Indels
  H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12;
WILSON K.J., JEFFERSON R.A.;
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H-T-H MOTIF (POTENTIAL).
6C1840FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000257; G1787904; -.
EMBL; D90805; G1742672; -.
ECOGENE; EG12667; UIDE.
PROSTIE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNN-BINDING; REPRESSOR.
DNA_BIND.
SEQUENCE 196 AA: "1700... H-T-H MOTIF 'Dominime."
 86 H-T-H MOTIF (POTE:
26204 MW; AD1F64FC CRC32;
                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                            UID OPERON REPRESSOR (GUS OPERON REPRESSOR).
                                                                                                                                                                                                                                                                                                  196 AA.
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SECT
                                                                                                                                                                                                      105 PTEKQYETLENQLAFLCQQ 123
                                                                                                                                                                                                                              166 RHAMQERTLQQ----FLCQR 181
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNKE
67
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                        UIDR OR GUSR
                                                                                                                                                                                                                                                                                              UIDR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12;
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES. HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTIE; PS00102; PHOSPHORYLASE; 1.
TRANSFERASE; GLYCOSYLTRANSFERASE; CARBOHYDRATE METABOLISM;
ALLOSTERIC ENIYME; PYRIDOXAL PHOSPHATE; TRANSIT PEPTIDE; CHLOROPLAST;
AMYLOPLAST; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches 67; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 KNKRALLDALAIEMLDRHHTHFCPLKGESWQDFLRNK----AKSFRCALLSHRNGAKVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 SDTRPTEKQYETLENQLAFLCQ----QGFSLENALYALSAVGHFT-----LGCVLEDQEH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: (1,4-ALPHA-D-GLUCOSYL)(N) + ORTHOPHOSPHATE = (1,4-ALPHA-D-GLUCOSYL)(N-1) + ALPHA-D-GLUCOSE 1-PHOSPHATE.
-! COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBCELLULAR LOCATION: CHLOROPLAST, AWYLOPLAST.
-!- SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
EMBL; M64362; G168276; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 ----TYDYYEKLNMKQAYYLSMEFLQGRALLNAIGNLELTGEYAEALNKLGHNLEN--- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSRL-----DKSKVINSALELLNEVGIEGL--TTRKLAQKLGV-EQPTLYWHV--- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSRLSGITPRARDDRSQFQNPRLEIAVPDRTAGLQRTKRTLLVKCVLDETKQTIQHVVTE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHLOROPLAST (POTENTIAL).
ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIN C.T., YEH K.W., LEE P.D., SU J.C.;
PLANT PHYSIOL. 0:0-0(1992).
-I- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
                                                                                                                                                                                                                                                                                                                                             (STARCH PHOSPHORYLASE L).
IPOMOBA BATATAS (SWEET POTATO) (BATATE).
SULANA, PLANTA, EMBRYOPHYTA, ANGIOSPERWAE; DICOTYLEDONEAE;
SOLANALES; CONVOLVUIACEAE.
                                                                                                                                                                                                                                                               01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ALPHA-GLÜCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (EC 2.4.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 86; DB 1; Length 955; 30.1%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86E3D50F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THII_SCHPO STANDARD; PRT; 577 AA. 009684; C1-NOY-1995 (REL, 32, CREATED) O1-NOY-1997 (REL, 35, LAST SEQUENCE UPDATE) O1-NOY-1997 (REL, 35, LAST ANNOTATION UPDATE) NUCLEAR FUSION PROTEIN THII.
                                                                                                                                                                                          955 AA.
                                                                                                                                                                                                                                      01-AUG-1992 (REL. 23, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             955 AA; 108520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 30.19
les 56; Conservative
                                                                                                                                                                                          STANDARD;
66 HFC-PLKGESWQDFL 79
                                                    73 RFREPIEGIHFVDYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 QVAKEE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 -VASKE 171
                                                                                                                                                                                       PHSL_IPOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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THT1_SCHPO
ID THT1_SC
AC 009684,
DT 01-NOV-
DT 01-NOV-
DT 01-NOV-
DE NUCLEAR
                                                                                                                                                           PHSL_IPOBA
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                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 SFKDINFRVNQEIMGLVELQNHQQEGMVQQKEILSTIKQLKSEIFDINSFFANFIEESAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 LENQLAFICQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEER----ETPTTDSMPP 168
                                                                                                                                                                                                                                                                                                                                                             37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           14 LELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHFCPLKGE 73
                                                                                                                                               DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAYONE F., NICLAS J., HOM-BOOHER N., SPARKS L., BERNSTEIN H.D., MCCAFEREY G., VALE R.D.;
J. CELL BIOL. 117:1263-1275(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                               Ouery Match
7.8%; Score 84.5; DB 1; Length 577;
Best Local Similarity 24.0%; Pred. No. 1.6;
Matches 49; Conservative 35; Mismatches 83; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
KNSI OR KNS.
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KULL F.J., SABLIN E.P., LAU R., FLETTERICK R.J., VALE R.D.;
NATURE 380:550-555(1996).
                                                                       IANGE Y., HORIO T., SHIMANUKI M., TANAKA K., NIWA O., SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94242426.
NICLAS J., NAVONE F., HOM-BOOHER N., VALE R.D.;
NEURON 12:1059-1072(1994).
THT1 OR SPACI3CS.03.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1-349.
MEDLINE; 96195066.
                                                                                                                                                                                                                                                                        POTENTIAL.
697D09FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   963 AA
                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 SVQSNID-FVNSGFQPLYDLTIQL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 LLRQAIELFDHQGAEPAFLFGLEL 192
                                                                                                                                                                                            EMBL; D87337; G1526454; -. EMBL; Z50112; G908892; ALT_INIT.
                                                                                                                                                                                                                                                                                      66972 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                           425
                                                                                                                                                                                                                                                                         491
                                                                                                                                                                                                                                                                        471 4
577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PLACENTA;
MEDLINE; 92299683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                            SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          405
                                                                                                                                                                                                                             TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINH_HUMAN
P33176;
                                                                                                                                        STRAIN-972;
                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                              RANSMEM
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308 NESETKSTLLFGQRAKTIKNTVCVNVELTAEOWKKKYEKEKEKNKILRNTIQWLENELNR 367
                                                                                                                                                                                                                                        93 HRNGAKVHSDTRPTEKQYETLENQL-AFLCQQGFSLEN--ALYALSAVGHFTLGCVLEDQ 149
                                                                                                                       248 LDEAKNINKSLSALGNVISALAEGSTYVPYRDSKMTRILQDSLGGNCRTTIVICCSPSSY 307
                                                                                4 LDKSKVINSALELLNEV---GIEGLT-----TRKLAQKLGVE-----QPTLY 42
                                                                                                                                                          43 WHVKNKRALLDALAIEMLDRHHTHFCPLKGESWQ------DFLRNKAKSFRCALLS 92
                                             45; Gaps
7.7%; Score 83.5; DB 1; Length 963; 25.0%; Pred. No. 3.8; tive 22; Mismatches 74; Indels 44
                                             47; Conservative
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          150 EHQVAKEE 157
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ERRKCEEE 424
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                 417
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Search completed: June 9, 1999, 13:01:03 Job time: 9122 sec

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OM protein '- protein search, using sw model

June 9, 1999, 13:00:33; Search time 28.57 Seconds Run on:

(without alignments)
399.721 Million cell updates/sec

Title:

Perfect score:

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Sequence:

BLOSUM62 Scoring table: 180763 seqs, 55169189 residues Searched:

SPTREMBL_8:* Database :

sp_fungi:* sp_human:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_organelle:*
sp_phage:*
sp_plant:*
sp_bacteria:*

sp_unclassified:* sp_vertebrate:* sp_rodent:*
sp_virus:*

sp_archea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q59466 haemophilus	21				067927 aquifex aeo	034643 bacillus su			295		P73186 synechocyst				Q51730 pseudomonas	P70477 rattus norv	3 ratt	Q13186 homo sapien	homo		Q42863 ipomoea bat	Q54830 streptococc	Q54835 streptococc	Q51516 pseudomonas	Q54719 streptococc			P96676 bacillus su
	-	TD	059466	053901	052558	034892	809650	067927	034643	053789	Q51597	053295	067157	P73186	087854	053310	007001	951730			013186							_		0037	P96676
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	1	Match Length	126	259	242	191	210	192	189	196	186	246	179	236	217	213	194	202	2472	2472	2477	435	185	340	488	581	202	539	216	4	198
æ	Query	Match	55.3	13.7	11.5	11.4	8.6	9.6	9.4	9.5	9.1	8.9	8.7	8.7			•	8.2	•	•					8.0	٠	8.0			7.7	7.7
	Ċ	score	597	147.5	124.5	123	105.5	103.5	102	66	98.5	œ.	94	93.5	93	91.5	91.5	89	88.5	88.5	86.5	86.5		98	98	86	86			83	
	Result	NO.	-	73	m	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

o	ď	0					51 025951 1		65 053165 1		631 Q90631	90 028306			38 P79138
O					4 01912		9 025951			9 00738	12 090631	_	9 P945	2 015087	4 P791
	192	405	542	207	285	285	235	215	187	82	1364	190	194	1520	369
188								ın	-	-*	-*	m	m	m	~
7.7 188	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7	7.4	7.1	7.1	7	7	7	7.3

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEUGE C., HICKMAN R.K., CURIALE M.S., HILLEN W., LEVY S.B.;
"Constitutive expression of tetracycline resistance mediated by a Tn10-11ke element in Haemophilus parainfluenzae results from a mutation in the repressor gene.";
J. BACTERIOL. 169:990-994 (1987).
-! SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS. ERBL; MIS539; G148989;
-. PROSITE: PS01081; HTH_TETR_FAMILY; 1.
PFRAM; PRO0440; tetr, 1.
RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                    01-NOV-1996 (TREMBLEEL. 01, CREATED)
01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
30S RIBOSOWAL PROTEIN S21.
HAEMOPHILUS PARAINFUGENZA.
BACTERIA, PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.3%; Score 597; DB 9; Length 12: 92.0%; Pred. No. 1.38-45; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
0RF1-4 (ACTII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AA; 14541 MW; 107F233B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA.
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.09
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 87137315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 COQGF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ANKVF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                  Q59466
Q59466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q53901
Q53901;
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RESULT
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                                          059466
                                                                              A PAC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
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AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEE--------RET 160
                                                                                                                                                                                                                                                                                                                                                                         58 EMLDRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPT-EKQYETLENQ 116
                                                                                                                                                                                                                                                                                                                                                                                              143 MNLLRSGGLHDELAAYGGDLLSTFVTAEALEQSSRNPGTEQGREQAGVFADQLHGYLKSL 202
                                                                                                                                                                                                                                                                                                               4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDAL ----AI 57
                                                                                                                                                                                                                                                                                                                                             31 LTQDRIVVTALGILDAEGLDALSMRRLAQELKTGHASLYAHVGNRDELLDLVFDIVLTEV 90
                                                                                                    FERNANDEZ MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F., "The act cluster contains regulatory and antibiotic export genes, direct targets for translational control by the blda tRNA gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W., TAYLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                             Length 259;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIRMICUTES; ACTINOBACTERIA; PSEUDONOCARDIACEAE;
                               BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G., J. BIOL. CHEM. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                          13.7%; Score 147.5; DB 9; 26.0%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 PTTDSMPPLLRQA--IELFDHQGAEPAFLFGLELIICGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 PAT-SFPNLVHLAGPITSLD---SDRRFELGLEIIIAGL 237
                                                                                                                                                Streptomyces.";
CELL 66:769-780(1991).
EMBL; M64683; G455360; -.
PPAM; PF00440; tetR; 1.
SEOUENCE 259 AA; 28268 MW; 16ECA071 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )570; G2792330; -.
242 AA; 27049 MW; 324EB570 CRC32;
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.0%; Pred. No. 1e-05
Matches 57; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, 01-AUG-1998 (TREMBLREL. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMYCOLATOPSIS MEDITERRANEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF040570; G2792330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
               STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEM. BIOL. 5:0-0(0002)
                                                                                          91347376.
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                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMYCOLATOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPRESSOR.
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11.5%; Score 124.5; DB 9; Length 242;

Query Match

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RAY ALLONI G., ALBERTENI A.M., ALLONI G., ALEVETNI A.M., ALLONI G., ALEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S., BORCHERT S., BORCHILES R., BOURSIER L., BRANK A., BRAUM M., BRIGHEL S.C., BRON S., BROULLIETS S., BRUGGHI C.V., CALDWELL B., CAPATER N.M., CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., EMBERSON P.T., EMENIAN K.D., ERRINGTON Y., FABRET C., FERRALI E., FOULGER D., FRITZ C., FARITZ C., EMENIAN K.D., ERRINGTON Y., FABRET C., FERRALI E., FOULGER D., FRITZ C., GRANDI G., GUISEPPI G., GALLERON N., GHIM S.Y., GARDER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G., GY B.J., HAGA K., HAIECH W.F., ITAYA M., JONES L., JORIS B., RARAMATA D., KASAHARA Y., KROH S., KUSANDI G., GUISEPPI G., GUISEPPI G., GOLSTER P., KONINGSTEIN G., KROH S., KUSANDI G., GUISEPI G., KASAHARA Y., KROH S., KUSANDI G., GUISEPI G., KASAHARA Y., KROH S., KONINGSTEIN G., KONINGS B., PARK S.H., PARKO V., POHL T.M., PORTETELLE D., RACHE B., REF MASUDE B., PARK S.H., PARKO V., POHL T.M., PORTETELLE D., RACHE B., REY M., SENONE G., KADANDI G., CANINAN E., SCHEDICH S., TAKAHASHI H., TAKAMARU K., TOGNONI A., TOSATO V., COLNYAMA R., TERPSTRA P., TOGNONI A., TOSATO V., COLNYAMA R., VANDENBOL M., WELLER RA, VANDERGER T., WINTER F., WINTER
                               7;
                                                                                                                                                                                 EM----LDRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSD----TRPTEKQY 110
                                                                                                                                                                                                                 138 --TECAQAVMACSPLPLKDRSAALNVVFQYVYGFTATESRWLEHLAETGRTAEEFAAEVT 195
                                                                                                                                                                                                                                                                                   111 ETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ---EHQV----AKEERETPTT 163
                                                                          2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRAL----LDALAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                          27 SELDREKIVATAVRVLDAEGDAKFSMRLLAEELNVTPMSVYWYVANKDDLLELALDAVAG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
  ; Pred. No. 0.00099; 35; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08, TRANSCRIPTION REGULATOR.
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 390:249-256(1997).
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      164 DSM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                   196 GSM 198
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                             Matches
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MEDLINE; 94254732.
PAN W., SPRATT B.G.;
"Regulation of the permeability of the gonococcal cell envelope by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 CIAODAADAEGGSWTVF-RHTLLHFFERLQSNDIYYKFH--------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 EH--TEONA--AVIAIA------RKHQAIWREKIT-----AVLTEAVENODLAD 155
                                                                                                                                                                                                                                                                                                                                 60 LDRHHTHFCPLKGES------WQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                                                                                      67 FDQMADSVTERKGDSAMLSLAHAYVDFAIENPGYYEAALL-----KVH-----DKRTE 114
                                                                                                                                                                                                                                                                                                                                                                                                             112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KEHLMLAALETFYRKGIARTSLNEIAQAAGVTRGALYWHFKNKEDLFDALFQRICDDIEN 71
                                                                                                                                                                       Query Match 11.4%; Score 123; DB 9; Length 191; Best Local Similarity 24.1%; Pred. No. 0.001; Matches 49; Conservative 38; Mismatches 74; Indels 42; Gaps
                                                                                                                                                                                                                                                     4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                                                                                6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. MICROBIOL. 11:769-775(1994).
-!- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%; Score 105.5; DB 9; Length 210; 26.8%; Pred. No. 0.039; tive 23; Mismatches 73; Indels 43
STRAIN-168;

KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

EMBL, AF027868; G2619045;

EMBL, Z99114; E1185379;

SEQUENCE 191 AA; 21016 MW; CB192356 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA; 24218 MW; E2FEDFC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 FSIR-----TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30S RIBOSOMAL PROTEIN S21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.8
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00440; tetR; 1. RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 225796; G438191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEISSERIA GONORRHOEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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RHHTHFCPLKGESWQDFLR------NKAKSFRCALLSHRNGAKVHSDTRPTEKQY 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 ETLENQ-----LAFLCQQGFSLENALY---ALSAVGHFTLGCVLEDQEHQVAKEER---- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GEVKNLPGELILKFL-----NGLYLKRKLKTYPEIALAVVTGSVERVFIFKERNFLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VF5;
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
EGRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL1-197) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENBL; AEO00776; G2984562; -.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
SEQUENCE 192 AA; 22259 MW; D2E83A94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNK----RALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                         DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 22.7%; Pred. No. 0.052;
Matches 45; Conservative 35; Mismatches 67; Indels 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                  01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                AOUIFEX AEOLICUS.
BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 AA
                                                                                                         192 AA
                                                                                                                                      01-AUG-1998 (TREMBLREL. 07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05,
05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 YDEETIKKELKKVLKSAI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 -- ETPTIDSMPPLLRQAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          NATURE 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                         PRELIMINARY;
                             156 DLDKETAVIF 165
179 HQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                STRAIN=VF5;
MEDLINE; 98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  034643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  034643
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                                                                                                         067927
                                                                                                                         067927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVKB
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034643
                                                                           RESULT
067927
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REPRESENT SERVICE 
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                                                                                                                                                                                                                                                                                            RA MUNSTERS, COGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORILLET S., BRUSCHI C.V., CALDWELL B., CAPUGNO V., CARTER N.M.,
RA BROUILLET S., BRUSCHI C.V., CANDRELL B., CAPUGNO N., CARTER N.M.,
RA BUTTAN K.D., ERRINGTON J.F., CONNERTON I.F., CHMINOS N.D., EMMERSON P.T.,
RA BUTTAN K.D., ERRINGTON J., FERRARI E., FOULGER D., FRITZ C.,
RA GLABER P., GOFFEAU A., GOLIGHILY E.J., GRANDI G., GUISEPPI G.,
RA HOLSAPPEL S., HOSONO S., HULLO M.F., ITARA M., JONES L., JORIS B.,
KARAMATA D., KASHARAR Y., KRORH S., KURAN M., KIEIN C., KOBAYASHI Y.,
RA HOLSAPPEL S., AGNONO S., HULLO M.F., ITARA M., JONES L., JORIS B.,
KARAMATA D., KASHARAR Y., KRORH S., KURAN M., KIEIN C., KOBAYASHI Y.,
RABILONOIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., ILU H.,
RABAINOIS S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
MOSSTL D., NAKAI S., NOBAGK M., NOONE D., O'RELLIK M., OGANA K.,
A GIWARA A., OUDEGA B., PARK S.H., PARKO V., POHL T. M., ORAN K.,
A GIWARA A., OUDEGA B., PARK S.H., PARKO V., POHL T. M., PRESCOTT A.M., PRESCAN E., PUJIC P., PURNELLE B.,
RACHE B., ROSE M., SADALE Y., SERIGUCHI M., TAKCHERIC S., SEROR S.J.,
A SERROR P., SHIN B.S., SOLDO B., SORONIN A., TRACHASHI H., TAKEMARU K., TAKEMARU K., TAKAHASHI H., TAKEMARU K., TAKAHASHI H., TAKEMARU K., TAKAHASHI H., TAKAHASHI H., TAKAHASHI H., TAKAHASHI H., TAKAHASHI H., TAMANOTO H., YAMANOTO H., YAMANOTO K., YANDERRE E.,
WANNIER F., VASSAROTI A., YARALOT A., YANDENBOL M.,
A VANNIER F., VASSAROTI A., YANDENBOL M.,
A VANNIER F., VOSHIDA K., YOSHIRAM H.F., ZUMSTEINE F.,
A TIPH COMDIETE GHORME CARRIED RANDEN STANDAN M., TOTAL M., TAKAHASHI R.,
A SOCHIE GHORME CARRIED RANDEN SA YANDER E.,
A SOCHIE GHORME CARRIED RANDEN SA YANDER E.,
A SOCHIE GHORME CARRIED RANDEN SA YANDER E.,
A WANDER F., VANDER F., VANDEN E.,
A SOCHIE G., YOSHIRAM H.F., ZONGYING CARRIED SA YANDER E.,
A SOCHIE GA CHOMIN A., TOSHIRAM H.F., ZUMSTEINE F.,
A SOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>``</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :::::|::|| : | | | |::|:| | : |::|| | : |::|| | : |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |:|| |:|| |:|| |:|| |:
LAZAREVIC V., SOLDO B., RIVOLTA C., REYNOLDS S., MAUEL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%; Score 102; DB 9; Length 189; 26.6%; Pred. No. 0.069; ative 27; Mismatches 36; Indels
                                                                                        SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITIED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF017113; G2618838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 299122; E1184436; -
PFAM; PF00440; tetr; 1.
SEQUENCE 189 AA; 21534 MW; 75FBEB90 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 HHTHFCPLKGESWQDFLRNKAKSFRCAL--LSHR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 HSSNRGSILEQTEGDLYKDLLHIGTCLLEELEHR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserve
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         MEDLINE; 98044033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
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                                              KARAMATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           053789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     053789
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053789
δŏ
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62 RHHTHFCPL-KGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTR----PTEKQYETLEN- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 DIITMLNRVGAGRARDDAVLVMAGAYRS--YAHHHPGRYSAFTRMPLGGDDPEYTAATRG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S AKLSRESIVEGALTFIDREGWDSLTINALATQLGTRGPSLYNHVDSLEDLRRAVRIRVID 64
                                                                                                                                                                                                                                                                                                                COLE S.T.; "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                             PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93326643.
ARANAKI H., KOGA H., SAGARA Y., HOSOI M., HORIUCHI T.;
Complete nucleotide sequence of the 5-exo-hydroxycamphor
dehydrogenase gene on the CAM plasmid of Pseudomonas putida (ATCC
17453).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLASMID CAM.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOGA H., ARAMAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T.,
GUNSALUS I.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "camR, a negative regulator locus of the cytochrome P-450cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%; Score 99; DB 9; Length 196; 25.8%; Pred. No. 0.13; tive 27; Mismatches 72; Indels
                                                                                                                                                                 COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                      HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                       PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL: AL021943; E1253107; -.
SEQUENCE 196 AA; 21262 MW; 17D86001 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ---- QLAFLCQQGFSLENALYAL----SAVGHFTL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydroxylase operon.";
J. BACIERIOL, 166:1089-1095(1986).
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01,
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Best Local Similarity 25.8%
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                     SEQUENCE FROM N.A.
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSEUDOMONAS PUTIDA.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               MEDLINE; 96181548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 86223770
MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAM REPRESSOR.
                                                                                                                                                 STRAIN=H37RV;
                                                       STRAIN-H37RV
                                                                                                                                                                                                                                             STRAIN=H37RV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PPG1;
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Q51597;
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97 DLLCSEKFRNIYFEKIEDAKRRFEKFLEKHFPSKAEILSEIILGFLRQLILHYVIKEERE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETL--ENQLAF---- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 --LCQQGF----SLENALYAL-----SAVGHFTLGCVLEDQEHQVAKEERE 159
                                            66 HFCP----LKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETL------ 114
                                                                                 91 AIFPSLDLATDSAREVIRRSVEEYVNLVDQHPNVLRVFIQGRSAKQSEATVRTLNEGREI 150
                                                                                                                                        114 ------ENQLAFLCQQGFSLENALYAL----------SAVGHF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KIISL ------FEENKEKTPEELL --------EMFLEVLYREKKVVYIFLF 96
                                                                                                                                                                                       151 TLAMAEMFNNELREMELNRAALELAAFAAFGSAASATEWWLGPEPDSPRRMPREQFVAHL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMEL/GENBANK/DDBJ DATA BANKS.
EMBL, AE000721; G2983549. .. E359173B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KERILEVSKELFFEKGYOGTSVEEIVKRANLSKGAFYFHFKSKEELI----TEIIERTHK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
32 RNEIVDAAFRAIDRLGPE-LSVRQIAEEAGTAKPKIYRHFTDKSDLLEAIGMRLRDMLWA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., CRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

8.7%; Score 94; DB 9; Length 179;
Best Local Similarity 21.4%; Pred. No. 0.33;
Matches 47; Conservative 33; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 TPTIDSMPPLLRQAIELFDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 LP---FLKEKLRE-------GLKLIFEGVKK 177
                                                                                                                                                                                                                                         141 T---LGCVLEDQEHQVAKEERETPTTDSMP--PLLR 171
                                                                                                                                                                                                                                                                                   211 TIIMMGVIVGTAEALGIAVDPDQPIHDAVPNNPAVR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
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                                                                                                                                                                                                                                                                                                                                                                                                        179 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 392:353-358(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VF5;
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P73186;
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P73186
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067157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
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                                                                                                     MEDLINE; 94304997.
ARAWAKI H., SAGARA Y., TAKEUCHI K., KOGA H., HORIUCHI T.;
"Mucleotide sequence of the gene encoding a repressor for the
cytochrome P-450cam hydroxylase operon on the Pseudomonas putida CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::::|: ||: | :| || :::|
4 KOSILHAAMRILSAKGRDGATMRPICAEVGVTPPTLYHHYGDLQGLHKAAIDETYRQVAE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKN----KRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.1%; Score 98.5; DB 9; Length 186; Best Local Similarity 29.8%; Pred. No. 0.14; Matches 25; Conservative 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
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EMBL; AL021287; E1237796; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA; 27618 MW; DC3E2076 CRC32;
                                                                                                                                                                                                                                                                                                                      SEQUENCE 186 AA; 20438 MW; 56E43196 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches
            BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 RHH---THFCPLKG--ESWQDFLR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 AYHGGTEERGPLKGIRDGWATFLO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYCOBACTERIUM TUBERCULOSIS
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                                                                                                                                                                                                                     EMBL; D14680; G473745; -. PFAM; PF00440; tetR; 1.
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                                                           SEQUENCE FROM N.A.
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                                                                                                                                     MEDLINE; 97061201.

KANEKO I., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA I.,
HOSOUCHI I., MATSUNO A., MURKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA I., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 CPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTERQYETLENQLAFLCQQGFSL 127
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136[1996).
                                                                                                                                                                                                                                                                                                                                                                                                      8 KVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHF
                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
                                                                                                                                                                                                                                                                                                                                                      8.7%; Score 93.5; DB 9; Length 236; 22.0%; Pred. No. 0.51; tive 22; Mismatches 59; Indels 4.
           01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 26.4 KD PROTEIN.
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                      TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEEGER R.J., HARRIS D.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 ENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 RENKYLLQV-----CFVEAQYHPELREKIQSEIIDKM 161
                                                                                                                                                                                                                                                                                                                  26384 MW; A8D84E37 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AA
                                                                                                                                                                                                                                                               EMBL; D90904; G1652269; -.
PROSTIE; PS001081; HTH_TETR_FAMILY; 1.
PFAM: PF00440; Lettr. 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 08, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TREMBLREL. 08, LAST SER OLINOV-1998 (TREMBLREL. 08, LAST SER PUTATIVE TRANSCRIPTIONAL REGULATOR. SC8A6.20C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 22.0 nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOMYCES COELICOLOR.
                                                                                                                                                                                                                                                                                                                    236 AA;
                                                                         SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
MEDLINE; 97000351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          087854
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; McD. MICROBIOL. 21:77-96(1996).
EMBL: AL031013; E1309426. ..
SEQUENCE 217 AA; 23650 MW; FBFEC38D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                      PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tubérculosis H37Rv, and comparison with Mycobacterium leprae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 RILGAAABLIALRGYSSTSTRDIAAAVGVEQPAIYKHFSAKRDILAALVRLAVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
                                                                                                                                                    Query Match 8.6%; Score 93; DB 9; Length 217; Best Local Similarity 37.9%; Pred. No. 0.51; Matches 22; Conservative 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "An integrated map of the genome of the tubercle bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           007001,
007001,
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
11-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; AL021646; E1248751; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN.
SEQUENCE 213 AA; 23120 MW; 2316B357 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.5%; Score 91.5; DE
Best Local Similarity 38.9%; Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL. 06, CREATED)
(TREMBLREL. 06, LAST SEQI
(TREMBLREL. 08, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TREMBLREL. 08, I
HYPOTHETICAL 23.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96181548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLE S.T
                                                                                                                                                                                                                                                                                                                                                                                          053310
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007001
AC 007001;
DT 01-JUL.
DT 01-NOV.
DE HYPOTHI
OS BACILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         007001
                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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RAY WINDLINE; SUGARARRA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BROUILLET S., BOURSTER L., BRANS A., BRAUN W., CARTER N.M.,
RA BROUILLET S., BOUNDERLE K.M., DUSTERHOUT B., CAPDANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA BRUIZOT F. DEVINE K.M., DUSTERHOUT A., ERILICHS S.D., EMMERSON P.T.,
RA GUTAM M., FUJITA Y., FUMA S., GALIZZI A., GALIERON N., GHIM S.Y.,
RA GUTABR P., KOSFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G.,
RAMARARA D., KASHARA Y., KLAERR-BLANCHARD M., KURITA K., LAIDER H.,
RAMARADA D., KASHARA Y., KLAERR-BLANCHARD M., KURITA K., LAPIDUS A.,
RA KOETTER P., KONINGSTEIN G., KOGMY S., KUMANO M., KURITA K., LADIDUS A.,
RA KOETTER P., MANJEL C., MEDIGUE C., PUJIC P., PURRELLE B.,
RA ROCHE B., ROSE M., SADAIE Y., SANDO T. O., O'RELLLY M., PORTETELE D.,
RA TAKAHAGII H., TAKEMANU K., TAKECH M., A' TAKAHAGII H., TAKEMANU K., TAKECH M., WAMBUT R., WEDLER R.,
WELTZENEGGER T., WINTERS P., WIPAT A., YAMANE R., YONGHE S., WIPAT K., YOSHIKAMA H., DANCHIN A.,
TORHOULLIS ".,
RA HARDING S., WOLL M., A' TOSATO V., UCHIYAMA H.F., ZUMSTEIN E.,
RA HERSDENDE P., WIPAT S., YOSHIRAMA H.F., ZUMSTEIN E.,
THE COMPLETE WE COMPLETE WE WINDE T., TOGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTH- 67
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 91.5; DB 9; Length 194; 22.6%; Pred. No. 0.6; tive 30; Mismatches 36; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LDQIKGRLHGDEDFWTVLDILIDET----FLITER----HKD-----
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SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BENEL: 294043; E313126; -.
EMBL: 299121; E1186136; -.
PFAM: PFO0440; tetR; 1.
SEQUENCE 194 AA: 22227 MW; D3457AEC CRC32;
                                                                                                                                                                                                             SUBMITIED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.6 Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 390:249-256(1997).
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103 VLCYSGLAIDHSM 115
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                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                         STRAIN=168
                                                 BACILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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